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From:

Jiang, Dong

Sent: To: Thursday, August 10, 2006 8:01 PM

STIC-Biotech/ChemLib

Subject:

10/735,149

Please search SEQ ID NO:28, and 27

- issued & Pub.
- commercial

Please send results on paper to Dong Jiang in REM 4D70 (mail stop REM 4C70).

Thank you very much.

Dong

Dong Jiang

AU1646 REM - 4D70 571-272-0872 Mail stop REM - 4C70

Searcher:
Searcher Phone:
Date Searcher Picked up:
Date completed:
Searcher Prep Time:
Online Time:

Type of Search

NA#______ AA#:_____

S/L:____ Oligomer:_____

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Structure #:____ Text:____

Inventor:_____ Litigation:____

Vendors and cost where applicable
STN:_____
DIALOG:___
QUESTEL/ORBIT:____
LEXIS/NEXIS:____
SEQUENCE SYSTEM:___
WWW/Internet:___
Other (Specify):____

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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-30
PRIOR FILING DATE: 2000-10-31
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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; SEQ ID NO 4436
; LENGTH: 623
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4436
                                                                                                 RESULT 5
US-09-522-217-1
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Matches
Patient No. 6307024
GENERAL INFORMATION:
APPLICANT: NO. 6307024ak, Julia E.
APPLICANT: Presnell, Scott R.
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GENERAL INFORMATION:
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Best Local Similarity
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                                                           Sequence 1, Application US/09522217
Patent No. 6307024
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APPLICANT: Foster, Donald C.
APPLICANT: Holly: Pichard D.
APPLICANT: Gross, Janet V.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Nelson, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LI
                                                                                                                    Sequence 1, Application Patent No. 6605272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 338; Conserv
                      APPLICANT:
APPLICANT:
APPLICANT:
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EARLIER FILING DATE: 199-07-01
NUMBER OF SEQ ID NOS: 115
SOPTWARE: FastSEQ for Windows Version
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CURRENT FILING DATE: 2000-03-09
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER FILING DATE: 1999-03-11
                                                                               APPLICANT: No. 6605272ak, Julia APPLICANT: Presnell, Scott R.
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ORGANISM: Homo :
FEATURE:
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                  : Presnell, Scott R.
: Sprecher, Cindy A.
: Foster, Donald C.
: Holly, Richard D.
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      Gross, Jane A.
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                     US-09-522-217-63
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US-10-295-723-63
US-09-949-016-4436
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US-10-295-723-1
US-10-282-622-1
US-10-282-622-1
US-10-282-622-1
US-10-282-622-1
US-10-282-622-217-84
US-09-522-217-84
US-09-522-217-3
US-10-295-723-846-3
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US-10-295-723-3
US-10-295-723-3
US-10-295-723-35
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US-09-949-016-12457	US-09-949-016-12029	US-09-949-016-15780	US-09-949-016-15144	US-09-949-016-4038	US-09-949-016-12561	US-09-949-016-158662	US-10-295-723-108	US-09-923-246-108	US-09-522-217-108	US-10-295-723-4	US-09-923-246-4	US-09-522-217-4	US-10-295-723-105	US-09-923-246-105	US-09-522-217-105	US-10-295-723-106	US-09-923-246-106	US-09-522-217-106	US-09-949-016-16178	US-10-295-723-88
Sequence 1, Appri Sequence 12457, A	Sequence 12029, A	Sequence 15780, A	Sequence 15144, A	Sequence 4038, Ap	Sequence 12561, A	Sequence 158662,	Sequence 108, App	Sequence 108, App	Sequence 108, App	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 105, App	Sequence 105, App	Sequence 105, App	Sequence 106, App	Sequence 106, App	Sequence 106, App	Sequence 16178, A	Sequence 88, Appl

ALIGNMENTS

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APPLICANT: No. 6307024ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Uniston, Andrew J.
APPLICANT: Nelson, Andrew J.
APPLICANT: Hillow, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAI1 LIGAND FILE REFERENCE: 99-16
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; ORGANISM: homo sapiens
US-09-522-217-63
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CURRENT FILING DATE: 2000-03-09
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER APPLICATION NUMBER: US 60/142,013
EARLIER APPLICATION NUMBER: US 60/142,013
EARLIER FILING DATE: 1999-07-01
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                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 63
LENGTH: 483
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                                                                                                                                                                                                                                  Best Local Similarity 84.1 Matches 338; Conservative
                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSEQ for Windows Version 3.0
124 AACTGTGAGTGGTCCGCTTTCTCCTGTTTCCAGAAAGCCCAGCTGAAATCCGCAAACACC 183
                                                                                           64 AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGGCTCCGGAAGATGTTGAGACC 123
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                                            AAAAATTATGTGAATGACTTGGTCCCTGAATTTCTGCCAGCTCCAGAAGATGTAGAGACA 201
                                                                                                                                            CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG
                                                                                                                                                                                                                                                         74.0%;
84.1%;
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Pred. No. 2.6e-87;
0; Mismatches 64
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APPLICANT: Nelson, Andrew J.

APPLICANT: Dillon, Stacey R.

APPLICANT: Dillon, Stacey R.

APPLICANT: Hammond, Angela K.

TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND

FILE REFERENCE: 99-16

CURRENT APPLICATION NUMBER: US/09/923,246

CURRENT FILING DATE: 2001-08-03

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217

PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09

PRIOR PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904

PRIOR PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013

PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 63
SEQ ID NO 63
LENGTH: 483
TYPE: DNA
ORGANISM: homo sapiens
US-09-923-246-63
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US-09-923-246-63
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Best Local S
Matches 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: No. 6605272ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
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ייח. 6605272
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                     184 GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAACGTAAACCGCCGTCC 243
                                                                                                     124 AACTGTGAGTGGTCCGCTTTCTCCTGTTTCCAGAAAGCCCAGCTGAAATCCGCAAACACC
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                                                                                                                                                                 AAAAATTATGTGAATGACTTGGTCCCTGAATTTCTGCCAGCTCCAGAAGATGTAGAGACA
                                                                                                                                                                                      AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGGCTCCGGAAGATGTTGAGACC
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                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                               74.0%;
84.1%;
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Pred. No. 2.6e-87;
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APPLICANT: OLORS, Datie A.

APPLICANT: OLORS, Date V.

APPLICANT: Nelson, Andrew J.

APPLICANT: Dillon, Stacey R.

APPLICANT: Dillon, Stacey R.

APPLICANT: Hammond, Angela K.

TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND

FILE REFERENCE: 99-16

CURRENT APPLICATION NUMBER: US/10/295,723

CURRENT FILING DATE: 2002-11-15

PRIOR APPLICATION NUMBER: 09/522,217

PRIOR APPLICATION NUMBER: US 60/123,547

PRIOR FILING DATE: 1999-03-09

PRIOR APPLICATION NUMBER: US 60/123,904

PRIOR APPLICATION NUMBER: US 60/123,904
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US-10-295-723-63
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 63
LENGTH: 483
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Best Local Similarity
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APPLICANT:
APPLICANT:
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APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      322
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304 AAAAAACCGCCGAAAGAATTCCTGGAACGTTTCAAATCCCTGCTGCAGAAAATGATTCAC 363
                                                                                                                                                                                                                                                                                                                                                   64 AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGGCTCCGGAAGATGTTGAGACC
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Sprecher, Cindy A.
Foster, Donald C.
Holly, Richard D.
                                                                            ACCAACGCAGGTCGTCGTCAGAAACACCGTCTGACCTGCCCGTCCTGTGATTCTTATGAG 303
                                                                                                                                                                      GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAAACTGAAAACGTAAAACCGCCGTCC
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                                             ACAAATGCAGGGAGAAGACAGAAAACACAGACTAACATGCCCCTTCATGTGATTCTTATGAG 381
                                                                                                                                       GGAAACAATGAAAGGATAATCAATGTATCAATTAAAAAGCTGAAGAGGAAACCACCTTCC
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milarity 84.1%;
Conservative (
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Pred. No. 2.6e-87;
0; Mismatches 64
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4436
LENGTH: 623
TYPE: DNA
ORGANISM: Human
US-09-949-016-4436
                                                                                    RESULT 5
US-09-522-217-1
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Sequence 1, Application US/09522217
Patent No. 6307024
GENERAL INFORMATION:
APPLICANT: No. 6307024ak, Julia E.
APPLICANT: Presnell, Scott R.
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Matches
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Pred. No. 2.9
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APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Janet V.
APPLICANT: Johnston, Janet V.
APPLICANT: Welson, Andrew J.
APPLICANT: Welson, Stacey R.
APPLICANT: Welson, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGHTLE REFERENCE: 99-16
CURRENT FILING DATE: 2000-03-09
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-01
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER FILING DATE: 1999-03-11
EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
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Local Similarity 84.1%;
Les 338; Conservative
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CAGCATCTGTCCTCTAGAACACACGGAAGTGAAGATTCCTGA
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; Sequence 1, Application US/0992324(
; Patent No. 6605272;
; GENERAL INFORMATION:
; APPLICANT: No. 6605272ak, Julia E
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.

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RESULT 6 US-09-923-246-1

US/09923246

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, NAME/KEY: CDS

, LOCATION: (47)...(532)
US-09-923-246-1
              APPLICANT: No. 6686178ak, Julia E. APPLICANT: Preenell, Scott R. APPLICANT: Sprecher, Cindy A. APPLICANT: Foster, Donald C. APPLICANT: Holly, Richard D. APPLICANT: Gross, Jane A. APPLICANT: Ohnston, Janet V. APPLICANT: Nelson, Andrew J. APPLICANT: Dillon, Stacey R.
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PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 642
                                                                                                                                                                                                               Sequence 1, Application Patent No. 6686178
                                                                                                                                                                                         GENERAL INFORMATION:
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Best Local :
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APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
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TYPE: DNA
ORGANISM: Homo &
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CURRENT FILING DATE: 2001-08-03
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Similarity 84.1%;
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Nelson, Andrew J.
Dillon, Stacey R.
Hammond, Angela K.
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Pred. No. 2.9e-87;
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CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: 09/522,217
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/123,547
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: 1999-03-11
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-01
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Best Local
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LOCATION: (47)...(532)
:-10-295-723-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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 494
                                     364
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                                                                                                                                                                                                                                                  GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAACGTAAACCGCCGTCC
                                                                                                                                                                                                                                                                                                                         AACTGTGAGTGGTCCGCTTTCTCCTGTTTCCAGAAAGCCCAGCTGAAATCCGCAAACACC 183
                                                                                                                                                                                                                                                                                                                                                                                                   AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGGCTCCGGAAGATGTTGAGACC 123
                                                                                                                                                                                                                                                                                                                                                                             AAAAATTATGTGAATGACTTGGTCCCTGAATTTCTGCCAGCTCCAGAAGATGTAGAGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 193
CAGCATCTGTCCTCTAGAACACACGGAAGTGAAGATTCCTGA
                                     CAGCACCTGTCCTCGTACCCACGGTTCCGAAGATTCCTGA 405
                                                                                                               AAAAAACCGCCGAAAGAATTCCTGGAACGTTTCAAATCCCTGCTGCAGAAAATGATTCAC
                                                                                                                                                  ACAAATGCAGGGAGAAGACAGAAACACAGACTAACATGCCCTTCATGTGATTCTTATGAG
                                                                                                                                                                                     ACCAACGCAGGTCGTCAGAAACACCGTCTGACCTGCCCGTCCTGTGATTCTTATGAG
                                                                                                                                                                                                                           GGAAACAATGAAAGGATAATCAATGTATCAATTAAAAAGCTGAAGAGGAAACCACCTTCC
                                                                                                                                                                                                                                                                                                     AACTGTGAGTGGTCAGCTTTTTCCTGTTTTCAGAAGGCCCCAACTAAAGTCAGCAAATACA
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84.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64;
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                                                                            493
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RESULT 8

US-10-282-622-1

; Sequence 1, Application US/10282622

; Patent No. 6929932
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
APPLICANT: West, James W.
APPLICANT: No. 6929932ak, Julia E.
APPLICANT: No. 6929932ak, Julia E.
TITLE OF INVENTION: ZALPHAII LIGAND ANTAGONISTS
; FILE REFERENCE: 01-37
; CURRENT FILING DATE: 2002-10-28
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/337,586
PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
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Wed

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APPLICANT: Presnell, Scott R.
APPLICANT: Holly, Richard D.
APPLICANT: Holly, Richard D.
APPLICANT: Nelson, Andrew J.
TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEITLE REFERENCE: 00-22
CURRENT APPLICATION NUMBER: US/09/825,561A
CURRENT EILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/194,731
PRIOR APPLICATION NUMBER: US 60/222,121
PRIOR FILING DATE: 2000-04-05
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 86
SOPTWARE: PRASTSEQ for Windows Version 3.0
SEQ ID NO 9
LENGTH: 486
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US-09-825-561A-9
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                                                          ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(486)
IS-09-825-561A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/09825561A Patent No. 6777539
Query Match
Best Local Similarity
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Best Local !
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (47)...(532)
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                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
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Similarity 84.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAAAACCGCCGAAAGAATTCCTGGAACGTTTCAAATCCCTGCTGCAGAAAATGATTCAC 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACTGTGAGTGGTCCGCTTTCTCCTGTTTCCAGAAAGCCCAGCTGAAATCCGCAAACACC 183
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     73.2%;
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   Score 296.6; DB 3; Pred. No. 2.4e-86;
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; NAME/KEY: CDS
; LOCATION: (1)...(489)
US-10-282-622-5
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US-10-282-622-5
                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 335; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/10282622 Patent No. 6929932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Presnell, Scott R.
APPLICANT: West, James W.
APPLICANT: No. 6929932ak, Julia E.
TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
FILE REFERENCE: 01-37
CURRENT APPLICATION NUMBER: US/10/282,622
CURRENT FILING DATE: 2002-10-28
                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/337,586
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                               FEATURE:
OTHER INFORMATION: zalphall ligand
                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                        FEATURE
                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                          124
                                                            148
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                                                                             64 AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGGCTCCGGAAGATGTTGAGACC 123
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               AACTGTGAGAGTGGTCCGCTTTCCCCTGTTTCCAGAAAGCCCCAGCTGAAATCCGCAAACACC 183
                                                                                                                                             CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGCACCTGTCCTCTCGTACCCACGGTTCCGAAGATTCC 402
                                                           AAAAATTATGTGAATGACTTGGTCCCTGAATTTCTGCCAGCTCCAGAAGATGTAGAGACA
                                                                                                                            CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGCATCTGTCCTCTAGAACACACGGAAGTGAAGATTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                           Conservative
                                                                                                                                                                                                      72.8%;
83.3%;
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                                                                                                                                                                                         Score 294.8; DB 3;
Pred. No. 9.4e-86;
0; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Migmatches
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                                                                                                                                                                                           67;
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                                                                                                                                                                                                                       Length
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US-09-522-217-84
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CURRENT FILING DATE: 2000-03-09
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: US 60/142,013
EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1560)
OTHER INFORMATION: MBP-human zalphall Ligand fusion polynucleotide
-09-522-217-84
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APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
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TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                              1225 TATGTGAATGACTTGGTCCCTGAATTTCTGCCAGCTCCAGAAGATGTAGAGACAAACTGT
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AACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAACGTAAAACGCCGTCCACCAAC
                                                                        GAGTGGTCAGCTTTTTCCTGTTTTCAGAAGGCCCAACTAAAGTCAGCAAATACAGGAAAC
                                                                                                 GAGTGGTCCGCTTTCTCCTGTTTCCAGAAAGCCCCAGCTGAAATCCCGCAAACACCGGTAAC 189
                                                                                                                                                                                                   TATGTGAATGACCTGGTTCCGGAATTCCTGCCGGCTCCGGAAGATGTTGAGACCAACTGT 129
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                                                                                                                                                                                                                                                                                                                                        Score 293.6; DB 3; Length 1560; Pred. No. 4.1e-85; 0; Mismatches 64; Indels 0;
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; FEATURE:
, NAME/KEY: CDS
; LOCATION: (1)...(1560)
; OTHER INFORMATION: MBP-human zalphall Ligand fusion
US-09-923-246-84
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Best Local Similarity
Matches 332; Conserv
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 84
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CURRENT APPLICATION NUMBER: US/09/923,246
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
PRIOR PELICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
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APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAll LIGAND
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH:
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                                                                                                                                               GAGTGGTCCGCTTTCTCCTGTTTCCAGAAAGCCCAGCTGAAATCCCGCAAACACCCGGTAAC 189
                                                                                                                                                                                                                           TATGTGAATGACCTGGTTCCGGAATTCCTGCCGGCTCCGGAAGATGTTGAGACCAACTGT 129
                                                                                                                                                                                                                                                                                                                CAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTGAAAAAT
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  GCAGGTCGTCAGAAACACCGTCTGACCTGCCCGTCCTGTGATTCTTATGAGAAAAAA 309
                                                                                                                                                                                                      TATGTGAATGACTTGGTCCCTGAATTTCTGCCAGCTCCAGAAGATGTAGAGACAAACTGT
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                                        AATGANAGGATAATCAATGTATCAATTAAAAAAGCTGAAGAGGAAACCACCTTCCACAAAT 1404
                                                                              AACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAACGTAAACCGCCGTCCACCAAC 249
                                                                                                                        GAGTGGTCAGCTTTTTCCTGTTTTCAGAAGGCCCCAACTAAAGTCAGCAAATACAGGAAAC 1344
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                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Pred. No. 4.1e-85;
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; NAME/KEY: CDS
; LOCATION: (1)...(1560)
; OTHER INFORMATION: MBP-human zalphall Ligand fusion polynucleotide
US-10-295-723-84
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US-10-295-723-84
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PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/123,547
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-01
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APPLICANT: No. 6686178ak,
APPLICANT: Presnell, Scol
APPLICANT: Sprecher, Cin
APPLICANT: Foster, Donal
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Sequence 84, Appir
Sequence 84, Appir
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APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND FILE REFERENCE: 99-16
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CURRENT FILING DATE: 2002-11-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1560
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 83.8 hes 332; Conservative
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                                                                                                                                        1285 GAGTGGTCAGCTTTTTCCTGTTTTCAGAAGGCCCAACTAAAGTCAGCAAATACAGGAAAC
                                                                                                                                                                                                                    1225 TATGTGAATGACTTGGTCCCTGAATTTCTGCCAGCTCCAGAAGATGTAGAGACAAACTGT
250 GCAGGTCGTCAGAAACACCGTCTGACCTGCCCGTCCTGTGATTCTTATGAGAAAAAA
                                                                                                                                                               130 GAGTGGTCCGCTTTTCTCCTGTTTTCCAGAAAGCCCAGCTGAAATCCGCAAACACCGGTAAC
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                                                                                   AACGAACGTATCATCAACGTTTCCATTAAAAAACGTGAAACGTAAACCGCCGTCCACCAAC 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gross, Jane A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Presnell, Scott R.
Sprecher, Cindy A.
Foster, Donald C.
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                                                                                                                                                                                                                                                                                                                                                                        Score 293.6; DB 3;
Pred. No. 4.1e-85;
0; Mismatches 64;
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                                                                                                                                                                                                                                                                                                                                                                                                             Length 1560;
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APPLICANT: No. 6307024ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Specher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Holly, Richard D.
APPLICANT: Johnston, Janet V.
APPLICANT: Uchnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
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CURRENT APPLICATION NUMBER: US/09/522,217
CURRENT FILING DATE: 2000-03-09
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: US 60/142,013
EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 225; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (1)...(486)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 486
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                        244
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                                                                                                                                                                                                                                                                        64 AAAAATTATGTGAATGACCTGGTTCCGGAAATTCCTGCCGGCTCCGGAAGATGTTGAGACC
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ACCAACGCAGGTCGTCAGAAACACCCGTCTGACCTGCCCGTCCTGTGATTCTTATGAG 303
                                                                                                                                                                           AACTGTGAGTGGTCCGCTTTCTCCTGTTTCCAGAAAGCCCAGCTGAAATCCGCAAACACC 183
                                                                                    GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAACGTAAACCGCCGTCC 243
                                                                                                                                                                                                                                                                                                                       AAYTGYGARTGGWSNGCNTTYWSNTGYTTYCARAARGCNCARYTNAARWSNGCNAAYACN
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                                                                  GGNAAYAAYGARMGNATHATHAAYGTNWSNATHAARAARYTNAARMGNAARCCNCCNWSN
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                                                                                                                                                                                                                                                                                                                                                                                                         71.8%; Score 290.6; DB 3; llarity 56.5%; Pred. No. 2.2e-84; Conservative 114; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Degenerate polynucleotide sequence zalphall ligand
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217

PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09

PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11

PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013

PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01

NUMBER OF SEQ ID NOS: 115

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 3

LENGTH: 486

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/923,246
CURRENT FILLING DATE: 2001-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: No. 6605272ak, Julia
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Poster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Degenerate polynucleotide sequence for human OTHER INFORMATION: zalphall ligand NAME/KBY: misc feature LOCATION: (1)...(466) OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
328
                                          244
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                                                                                                                                                                                                          124 AACTGTGAGTGGTCCGCTTTCTCCTGTTTCCAGAAAGCCCAGCTGAAATCCCGCAAACACC 183
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                       ACCAACGCAGGTCGTCGTCAGAAACACCGTCTGACCTGCCCGTCCTGTGATTCTTATGAG 303
                                                                                  GUNAAYAAYGARMGNATHATHAAYGTNWSNATHAARAARYTNAARMGNAARCCNCCNWSN 327
                                                                                                                     GGTAACAACGAACGTATCAATCAACGTTTCCATTAAAAAAACTGAAACGTAAAACCGCCGTCC 243
                                                                                                                                                                           AAYTGYGARTGGWSNGCNTTYWSNTGYTTYCARAARGCNCARYTNAARWSNGCNAAYACN 267
                                                                                                                                                                                                                                                                     ||:||:||:||:||:||:||:||:|| 207
                                                                                                                                                                                                                                                                                                                  AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGGCTCCGGAAGATGTTGAGACC 123
                                                                                                                                                                                                                                                                                                                                                            CARGGNCARGAYMGNCAYATGATHMGNATGMGNCARYTNATHGAYATHGTNGAYCARYTN
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ACNAAYGCNGGNMGNMGNCARAARCAYMGNYTNACNTGYCCNWSNTGYGAYWSNTAYGAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative 114; Mismatches
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Search completed: August 7, 2006, 12:12:48
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seq length:
Published Applications NA Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*

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8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*

10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*

11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*

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13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*

14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*

15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*

16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*
                                                                                       IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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73.6	73.6	74.0	74.0	74.0	74.0	74.0	74.0	74.0	74.0	74.0	74.0	74.0	74.0	74.0	74.0	Query Match
617	611	642	642	642	642	642	642	642	642	642	489	483	483	483	483	Length [
9 1	16	15	13	10	9	ω	7	7	7	w	10	φ	œ	7	ω	DB BG
US-10-264-634-18	US-11-137-807-11	US-11-134-489-1	US-11-174-398-1	US-10-951-239-1	US-10-787-442-1	US-10-659-684-1	US-10-456-780-1	US-10-282-622-1	US-10-295-723-1	US-09-923-246-1	US-10-775-204-2157	US-10-787-442-63	US-10-659-684-63	US-10-295-723-63	US-09-923-246-63	ID
Sequence 18, Appi Sequence 18, Appl	11,	Sequence 1, Appli	Sequence 1, Appli	ب	Sequence 1, Appli	Sequence 1, Appli	Ļ	Sequence 1, Appli	1,	Sequence 1, Appli	Sequence 2157, Ap	Sequence 63, Appl	Sequence 63, Appl	Sequence 63, Appl	Sequence 63, Appl	Description

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82 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG

141

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18
182	182	182	252.8	254.4	254.4	256	256	259.8	261.4	264.4	264.4	290.6	290.6	290.6	290.6	293.6	293.6	293.6	293.6	294.8	294.8	296.6	296.6	296.6	298	298	298
44.9	44.9	44.9	62.4	62.8	62.8	63.2	63.2	64.1	64.5	65.3	65.3	71.8		71.8	71.8	72.5	72.5	72.5	72.5	72.8	72.8	73.2	73.2	73.2	73.6	73.6	73.6
3072	3072	3072	393	393	393	393	393	399	399	444	444	486	486	486	486	1560	1560	1560	1560	489	489	486	486	399	617	617	617
7	w	w	10	10	10	10	10	10	10	13	7	9	8	7	w	9	80	7	w	13	7	9	w	10	16	16	œ
US-10-295-723-55	US-09-825-561A-46	US-09-923-246-55	US-10-867-992-1	US-10-867-992-7	US-10-867-992-5	US-10-867-992-9	US-10-867-992-3	US-10-867-992-13	US-10-867-992-11	US-11-174-398-3	US-10-282-622-3	US-10-787-442-3	US-10-659-684-3	US-10-295-723-3	US-09-923-246-3	US-10-787-442-84	US-10-659-684-84	US-10-295-723-84	US-09-923-246-84	US-11-174-398-5	US-10-282-622-5	US-10-872-087-9	US-09-825-561A-9	US-10-867-992-18	US-11-197-488-18	US-11-132-947-1	US-10-620-169-1
Sequence 55, Appl	46,		۳	Sequence 7, Appli	<u>ა</u>	,	ω '	Sequence 13, Appl	11,	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	ω •	Sequence 3, Appli	84,	-	-	Sequence 84, Appl	Sequence 5, Appli	Sequence 5, Appli		Þ	Sequence 18, Appl	Sequence 18, Appl	Sequence 1, Appli	Sequence 1, Appli

ALIGNMENTS

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APPLICANT: JOHNSTON, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Dillon, Stacey R.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/923,246
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/
PRIOR FILING DATE: BARLIER FILING DATE: 2000-03-09
PRIOR FILING DATE: BARLIER FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/
PRIOR FILING DATE: BARLIER FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/
PRIOR APPLICATION NUMBER: US/
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US-09-923-246-63
; Sequence 63, Application US/09923246
; Patent No. US20020128446A1
                      S
                                                                                                                                                                                                                                                                            ; TYPE: DNA; ORGANISM: homo sapiens US-09-923-246-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ
SEQ ID NO 63
                                                                                                                  Matches
                                                                                                                                                     Query Match
Best Local Similarity
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APPLICANT: Pres
APPLICANT: Spre
APPLICANT: FOSS
APPLICANT: HOLI
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                                                                                                              338;
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4 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Foster, Donald C. Holly, Richard D. Gross, Jane A.
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                                                                                                                  Conservative
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                                                                                                                                                     74.0%;
84.1%;
                                                                                                              <u>.</u>
                                                                                                              Score 299.6; DB 3;
Pred. No. 1.5e-87;
0; Mismatches 64;
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                                                                                                                                                                                                                      ; LENGTH: 483
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-295-723-63
                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/10/295,723
CURRENT FILLING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: 09/522,217
PRIOR FILING DATE: 2000-03-09
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: US 60/123,547
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: 1999-03-11
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US-10-295-723-63
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                                                                                                                                                 Matches
                                                                                                                                                                                    Query Match
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: No. US20030125524Alak,
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                    Local Similarity
 142
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                                                                                                                                                 338;
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                                    64 AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGGCTCCGGAAGATGTTGAGACC 123
                                                                                                          4.
                                                                                           CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGAATATTGTTGATCAGCTG
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Dillon, Stacey R.
                                                                                                                                                 Conservative
                                                                                                                                                              74.0%;
84.1%;
                                                                                                                                               0; Mismatches
                                                                                                                                                                  Score 299.6;
Pred. No. 1.5
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                                                                                                                                                                  .5e-87;
                                                                                                                                                                                    DB 7;
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                                                                                                                                                 Indels
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                                                                                                                                               Gaps
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RESULT 3
US-10-659-684-63
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SOPTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Novak, J.
APPLICANT: Presnel
                                                                                                                                                                                                                                                                               Query Match
Best Local
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Publication No.
                                                                                                                                                                                                                                                              Matches
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APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND FILE REFERENCE: 99-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/659,684
CURRENT FILING DATE: 2003-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US/09/522,217 PRIOR FILING DATE: 2000-03-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: homo
                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 483
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                                                                                                              142
                                                                                                                                  64 AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGGCTCCGGAAGATGTTGAGACC 123
                                                                                                                                                                                                                                                              338;
                                                                                                                                                                                     82
                                                                                                                                                                                                        4 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 63
                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Presnell, Scott R.
Sprecher, Cindy A.
Foster, Donald C.
Holly, Richard D.
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 GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAACGTAAACCGCCGTCC 243
                                                                        AACTGTGAGTGGTCCGCTTTCTCCTGTTTCCAGAAAGCCCAGCTGAAATCCCGCAAACACC 183
                                                                                                             AAAAATTATGTGAATGACTTGGTCCCTGAATTTCTGCCAGCTCCAGAAGATGTAGAGACA
                                                                                                                                                                                   CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG
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                                      AACTGTGAGTGGTCAGCTTTTTCCTGTTTTCAGAAGGCCCAACTAAAGTCAGCAAATACA
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No. US20040110932A1
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84.1%;
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Pred. No. 1.5e-87;
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US-10-787-442-63
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US-10-787-442-63
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Publication No.
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Best Local Similarity
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PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/123,547
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/142,013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/10/787,442
CURRENT FILING DATE: 2004-02-26
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APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Novak, Julia E.
APPLICANT: Presnell, Scot
APPLICANT: Sprecher, Cind
APPLICANT: Foster, Donald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 483
                    244
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Sprecher, Cindy A.
Foster, Donald C.
Holly, Richard D.
Gross, Jane A.
Tobactor Teat V.
ACCAACGCAGGTCGTCAGAAACACCGTCTGACCTGCCCGTCCTGTGATTCTTATGAG
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                                                                                                                  AACTGTGAGTGGTCAGCTTTTTCCTGTTTTCAGAAGGCCCCAACTAAAGTCAGCAAATACA
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84.1%;
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Pred. No. 1.5e-87;
0; Mismatches 64;
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CURRENT FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/341,811
PRIOR FILING DATE: 2001-12-21
PRIOR PPLICATION NUMBER: 60/360,000
PRIOR FILING DATE: 2002-02-28
PRIOR PPLICATION NUMBER: 60/378,950
PRIOR FILING DATE: 2002-05-10
PRIOR FILING DATE: 2002-05-10
PRIOR PRILING DATE: 2002-07-24
PRIOR PPLICATION NUMBER: 60/411,355
PRIOR APPLICATION NUMBER: 60/414,984
PRIOR FILING DATE: 2002-10-02
PRIOR PPLICATION NUMBER: 60/417,611
PRIOR APPLICATION NUMBER: 60/47,611
PRIOR APPLICATION NUMBER: 60/47,611
PRIOR APPLICATION NUMBER: 60/47,611
PRIOR APPLICATION NUMBER: 60/420,246
PRIOR FILING DATE: 2002-10-11
PRIOR PILING DATE: 2002-10-23
PRIOR APPLICATION NUMBER: 60/420,246
PRIOR APPLICATION NUMBER: 60/420,246
PRIOR APPLICATION NUMBER: 60/420,246
PRIOR APPLICATION NUMBER: 60/420,246
PRIOR PILING DATE: 2002-10-23
PRIOR PILING DATE: 2002-10-23
PRIOR PRILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/423,623
PRIOR PILING DATE: 2002-01-28
PRIOR FILING DATE: 2002-01-28
PRIOR FILING DATE: 2002-01-28
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US-10-775-204-2157
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SEQ ID NO 2157
LENGTH: 489
TYPE: DNA
ORGANISM: Hom
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APPLICANT: Haseltine,
APPLICANT: Balance, Da
APPLICANT: Turner, And
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APPLICANT: Turner, Andrew J.
TITLE OF INVENTION: Albumin Fusion Proteins
268
                                          184
                                                                                                                                 124
                                                                                                                                                                              148 AAAAATTATGTGAATGACTTGGTCCCTGAATTTCTGCCAGCTCCAGAAGATGTAGAGACA
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                                                                                                                   AACTGTGAGTGGTCCGCTTTCTCCTGTTTCCAGAAAGCCCAGCTGAAATCCGCAAACACC
                                                                                    AACTGTGAGTGGTCAGCTTTTTCCTGTTTTCAGAAGGCCCAACTAAAGTCAGCAAATACA
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GGAAACAATGAAAGGATAATCAATGTATCAATTAAAAAAGCTGAAGAGGAAACCACCTTCC
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Pred. No. 1.5e-87;
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US-09-923-246-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
PRIOR PILING DATE: EARLIER FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND FILE REFERENCE: 99-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .09-923-246-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo
FEATURE:
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APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
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CURRENT FILING DATE: 2001-08-03
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LOCATION: (47)...(532)
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                       ACCAACGCAGGTCGTCGTCAGAAACACCGTCTGACCTGCCCGTCCTGTGATTCTTATGAG 303
                                                                                                                               GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAAACTGAAACGTAAACCGCCGTCC 243
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                                                                                                                                                                                                                                                                     AAAAATTATGTGAATGACTTGGTCCCTGAATTTCTGCCAGCTCCAGAAGATGTAGAGACA
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ACAAATGCAGGGAGAAGACAGAAACACAGACTAACATGCCCTTCATGTGATTCTTATGAG
                                                                                   GGAAACAATGAAAGGATAATCAATGTATCAATTAAAAAGCTGAAGAGGAAACCACCTTCC
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84.1%;
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Pred. No. 1.7e-87;
0; Mismatches 64;
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US-10-295-723-1
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US-10-295-723-1
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CURRENT APPLICATION NUMBER: US/10/295,723
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: 09/522,217
PRIOR PPLICATION NUMBER: 09/522,217
PRIOR PPLICATION NUMBER: US 60/123,547
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR PILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR PILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/142,013
PRIOR PILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-01
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APPLICANT:
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TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
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Sprecher, Cindy A.
Foster, Donald C.
Holly, Richard D.
AAAAAACCGCCGAAAGAATTCCTGGAACGTTTCAAATCCCTGCTGCAGAAAATGATTCAC 363
                                                                              ACCAACGCAGGTCGTCGTCAGAAACACCGTCTGACCTGCCCGTCCTGTGATTCTTATGAG 303
                                                                                                                                                   GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAACGTAAACCGCCGTCC
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                                                                                                                                                                                                                                                                                             AAAAATTATGIGAATGACCTGGTTCCGGAAATTCCTGCCGGCTCCGGAAGATGTTGAGACC
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                                                         ACAAATGCAGGGAGAAGACAGAAACACAGACTAACATGCCCTTCATGTGATTCTTATGAG
                                                                                                                             GGAAACAATGAAAGGATAATCAATGTATCAATTAAAAAGCTGAAGAGGAAAACCACCTTCC
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Nelson, Andrew J.
Dillon, Stacey R.
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84.1%;
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Pred. No. 1.7e-87;
0; Mismatches 64;
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RESULT 9
US-10-456-780-1
Sequence 1, Application US/10456780
Publication No. US20040009150A1
GENERAL INFORMATION:
APPLICANT: Helson, Andrew J.
APPLICANT: Hughes, Steven D.
APPLICANT: Holly, Richard D.
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APPLICANT: Presnell, Scott R.

APPLICANT: West, James W.

APPLICANT: No. US20030134390Alak, Julia E.

TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS

FILE REFERENCE: 01-37

CURRENT APPLICATION NUMBER: US/10/282,622

CURRENT FILING DATE: 2002-10-28

PRIOR APPLICATION NUMBER: 60/337,586

PRIOR FILING DATE: 2001-11-05

NUMBER OF SEQ ID NOS: 30
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US-10-282-622-1
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Best Local S
Matches 338
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Publication No. US20030134390A1
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ORGANISM: Homo
FEATURE:
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nilarity 84.1%;
Conservative
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                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Novak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Sillon, Andrew J.
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                    APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hillon, Stacey R.
APPLICANT: Hommond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIVERITE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/10/659,684
CURRENT FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: US/09/522,217
PRIOR APPLICATION DATE: 2000-03-09
PRIOR FILING DATE: 2000-03-09
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-10-659-684-1
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; NAME/KEY: CDS
; LOCATION: (47)...(532)
US-10-456-780-1
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Best Local Similarity
Matches 338; Conserv
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                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/10659684 Publication No. US20040110932A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: USE OF IL-21 IN CANCER AND TITLE OF INVENTION: OTHER THERAPEUTIC APPLICATIONS FILE REFERENCE: 03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo
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          APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  494
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Pred. No. 1.7e-87;
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            US 60/123,547
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243 313

493 363 433 303 373

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Sequence 1, Application US/10787442
Publication No. US20040260065A1
GENERAL INFORMATION:
APPLICANT: NOVAK, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Holly, Richard D.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Nelson, Stacey R.
APPLICANT: Dillon, STACEY R.
FILE REFERENCE: 99-16
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 642
TYPE: DNA
ORGANISM: Homo sapiens
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; NAME/KEY: CDS
; LOCATION: (47)...(532)
US-10-659-684-1
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US-10-787-442-1
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                                                               CURRENT APPLICATION NUMBER: US/10/787,442
CURRENT FILING DATE: 2004-02-26
PRIOR APPLICATION NUMBER: US/09/522,217
PRIOR FILING DATE: 2000-03-09
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                     APPLICATION NUMBER: US 60/123,547 FILING DATE: 1999-03-09
APPLICATION NUMBER: US 60/123,904
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84.1%;
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Pred. No. 1.7e-87;
0; Mismatches 64;
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DATE: 1999-03-11
APPLICATION NUMBER: US 60/142,013
DATE: 1999-07-01
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US-10-951-239-1
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                                                                                                     CURRENT APPLICATION NUMBER: US/10/951,239
CURRENT FILING DATE: 2004-09-27
PRIOR APPLICATION NUMBER: 60/505,919
PRIOR FILING DATE: 2003-09-25
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/10951239
Publication No. US20050095223A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/142,01
PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1
LENGTH: 642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                            APPLICANT: Sivakumar, Pallavur
APPLICANT: Nelson, Andrew
TITLE OF INVENTION: METHODS OF TREATING AUTOIMMUNE DISEASES
TITLE OF INVENTION: USING IL-21
FILE REFERENCE: 03-09
FILE REFERENCE: 03-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1999-03-11
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ORGANISM: Homo
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LOCATION: (47)...(532)
NAME/KEY: CDS
LOCATION: (47
                                                   ORGANISM: Homo
                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                  FEATURE:
                                                                                      LENGTH: 642
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Pred. No. 1.7e-87;
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Query Match

74.0%;

Score 299.6;

DB 10;

Length 642;

303

493 363 243

373

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APPLICANT: Presnell, Scott R.
APPLICANT: West, James W.
APPLICANT: Novak, Julia E.
TITLE OF INVENTION: ZALPHAII LIGAND ANTAGONISTS
FILE REFERENCE: 01-37
CURRENT APPLICATION NUMBER: US/11/174,398
CURRENT FILING DATE: 2005-07-01
PRIOR APPLICATION NUMBER: US/10/282,622
PRIOR APPLICATION NUMBER: US/10/282,622
PRIOR FILING DATE: 2002-10-28
PRIOR PILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: 60/337,586
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
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US-11-174-398-1
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                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 1
                                                                                                                                                                                               Matches
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Matches 338; Conservative
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Best Local
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                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo
FEATURE:
                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: (47)...(532)
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cal Similarity 84.1%;
338; Conservative
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                                                                          AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGGCTCCGGAAGATGTTGAGACC
                                                                                                                         CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG
 AACTGTGAGTGGTCCGCTTTCTCCTGTTTCCAGAAAGCCCAGCTGAAATCCGCAAACACC
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                                                        AAAAATTATGTGAATGACTTGGTCCCTGAATTTCTGCCAGCTCCAGAAGATGTAGAGACA
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US-11-134-489-1
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Best Local S
Matches 338
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CURRENT APPLICATION NUMBER: US/11/134,489
CURRENT FILING DATE: 2005-05-20
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Kindavogel, Wayne R.
APPLICANT: Holly, Richard D.
APPLICANT: Holly, Richard D.
APPLICANT: Clegg, Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/11134489 Publication No. US20050265966A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: .....Sivakumar, Pallavur V.
TITLE OF INVENTION: METHODS OF TREATING CANCER USING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: (47)...(532)
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r: Holly, Richard D.
r: Clegg, Christopher H.
r: Foster, Donald C.
r: Johnson, Rebecca A.
r: Heipel, Mark D.
                                                                                                                                                                                                                                                                                    AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGGCTCCGGAAGATGTTGAGACC
AAAAAACCGCCGAAAGAATTCCTGGAACGTTTCAAATCCCTGCTGCAGAAAATGATTCAC
                                                                        ACCAACGCAGGTCGTCGACAAAACACCGTCTGACCTGCCCGTCCTGTGATTCTTATGAG
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Pred. No. 1.7e-87;
0; Mismatches 64;
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303

373 243

433

313

183

253 123 193 63

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NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.3
SEQ ID NO 11
LENGTH: 611
TYPE: DNA
ORGANISM: Homo sapiens
US-11-137-807-11
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US-11-137-807-11
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Search completed: August Job time: 1012 secs
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Publication No. US20060034810A1
GENERAL INFORMATION:
APPLICANT: Riley, James
APPLICANT: Vonderheide, Robert
APPLICANT: Vonderheide, Robert
APPLICANT: Vonderheide, Robert
APPLICANT: Vonderheide, Robert
APPLICANT: Schoski, Megan
TITLE OF INVENTION: NOVEL ARTIFICIAL ANTIGEN PRESENTING CELLS AND USES THEREFOR
FILLE REFERENCE: 053893-5054US1
CURRENT APPLICATION NUMBER: US/11/137,807
CURRENT ELING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/575,712
PRIOR FILING DATE: 2004-05-27
NUMBER OF SECT TO NOC. 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 337; Conserv
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                                                                                                                                                            304 AAAAAACCGCCGAAAGAATTCCTGGAACGTTTCAAATCCCTGCTGCAGAAAATGATTCAC 363
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                7,
                2006, 12:30:07
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Copyright

GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.

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Result
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417.070 Million cell updates/sec
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| MMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
| MMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
| MMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
| MMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
| MMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
| MMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
| MMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
| MMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
| MMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
| MMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
| MMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
| MMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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Maximum Match 100%
Listing first 45 summaries
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US-11-266-748A-472688

US-11-266-748A-472688

US-10-806-611-1

US-10-806-611-3

US-10-735-149-26

US-10-735-149-17

US-10-735-149-18

US-10-735-149-19

US-10-735-149-19

US-10-735-149-19

US-10-735-149-20

US-10-735-149-21

US-10-735-149-21

US-10-735-149-21

US-10-735-149-15

US-10-735-149-15

US-10-735-149-11

US-10-735-149-11

US-10-735-149-11

US-10-735-149-11

US-10-735-149-11

US-10-735-149-11

US-10-735-149-11

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US-10-735-149-11
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US-10-511-937-565
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Sequence 472688,
Sequence 472688,
Sequence 1, Appli
Sequence 26, Appli
Sequence 26, Appli
Sequence 18, Appli
Sequence 19, Appli
Sequence 19, Appli
Sequence 19, Appli
Sequence 22, Appli
Sequence 21, Appli
Sequence 15, Appli
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Sequence 17, Appli
Sequence 18, Appli
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Sequence 14, Appli
Sequence 16, Appli
Sequence 17, Appli
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Sequence 19, Appli
Sequence 10, Appli
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Sequence
Sequence
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Sequence 565, App
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7.7	7.9	7.9	7.9	7.9	7.9	7.9	7.9	7.9	7.9	7.9	7.9	7.9	8.0	8.0	8.0		8.0	8.0	8.0	8.0	8.0
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
159, App	65372, A	62533, A	20672, A	227053,	467013,	395967,	337116,	285687,	58700, A	241212,	227054,	193446,	29566, A	2827, Ap	249298,	219123,	138074,	85263, A	44600, A	332293,	2/1//6,

ALIGNMENTS

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RESULT 1

US-10-735-149-27

Sequence 27, Application US/10735149

Publication No. US20060134754A1

GENERAL INFORMATION:
APPLICANT: Chan, Chung
APPLICANT: Zamost, Bruce L.
APPLICANT: Covert, Douglas C.
APPLICANT: Liu, Hong Y.
APPLICANT: Dough, Karen S.
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                                                                                                                                                                                                                                                                                                                                    ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(405)
US-10-735-149-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Meyer, Jeffrey D.
APPLICANT: Holderman, Susan D.
TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21
TITLE OF INVENTION: IN A PROKARYOTIC HOST
FILE REFERENCE: 02-12
CURRENT APPLICATION NUMBER: US/10/735,149
CURRENT FILING DATE: 2003-12-12
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 27
LENGTH AC
                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 405; DB 6; I Best Local Similarity 100.0%; Pred. No. 3.4e-127;
                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: optimized IL-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 405
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121 ACCAACTGTGAGTGGTCCGCTTTCTCCTGTTTCCAGAAAGCCCCAGCTGAAATCCGCAAAC 180
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                                                             CTGAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGGCTCCGGAAGATGTTGAG
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120 120 60 60

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PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR PILLING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILLING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 565
LENGTH: 642
TYPE: DNA
ORGANISM: Homo sapiens
US-10-511-937-565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
APPLICANT: Wohlgemuth, Jay
APPLICANT: Wrik
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT FILING DATE: 2004-10-19
CURRENT FILING DATE: 2004-10-19
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                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 74.0%;
Best Local Similarity 84.1%;
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                                                                                                                                                                                                                                                                   64 AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGGCTCCGGAAGATGTTGAGACC 123
                                                                                                                                                                                                                                                                                                                                                                      4
                       ACCAACGCAGGTCGTCGGAAAACACCGTCTGACCTGCCCGTCCTGTGATTCTTATGAG 303
                                                                                                   GGTAACAACGAACGTATCAACGTTTCCATTAAAAAACTGAAACGTAAACGGCCGTCC
                                                                                                                                                              AACTGTGAGTGGTCAGCTTTTTCCTGTTTTCAGAAGGCCCAACTAAAGTCAGCAAATACA 313
                                                                                                                                                                                       AACTGTGAGTGGTCCGCTTTCTCCTGTTTCCAGAAAGCCCCAGCTGAAATCCCCAAACACC 183
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ACAAATGCAGGGAGAAGACAGAAACACAGACTAACATGCCCTTCATGTGATTCTTATGAG
                                                                              GGAAACAATGAAAGGATAATCAATGTATCAATTAAAAAAGCTGAAGAAGGAAACCACCTTCC
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (47)...(535)
US-10-735-149-1
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APPLICANT: Chan, Chu
APPLICANT: Zamost,
APPLICANT: Covert,
APPLICANT: Liu, Hon
APPLICANT: De Jongh
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APPLICANT: Holderman, Susan D.
TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21
TITLE OF INVENTION: IN A PROKARYOTIC HOST
FILE REFERENCE: 02-12
CURRENT PELLICATION NUMBER: US/10/735,149
CURRENT FILING DATE: 2003-12-12
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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                    CAGCACCTGTCCTCTCGTACCCACGGTTCCGAAGATTCCTGA 405
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                                                                                              AAAAAACCGCCGAAAGAATTCCTGGAACGTTTCAAATCCCTGCTGCAGAAAATGATTCAC 363
                                                                                                                                                                 ACCAACGCAGGTCGTCGTCAGAAACACCGTCTGACCTGCCCGTCCTGTGATTCTTATGAG 303
                                                                                                                                                                                                                                             GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAACGTAAACCGCCGTCC 243
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CAGCATCTGTCCTCTAGAACACACGGAAGTGAAGATTCCTGA
                                                                      ÁAAAAACCACCCAAAGAATTCCTAGAAAGATTCAAATCACTTCTCCAAAAGATGATTCAT 493
                                                                                                                                           ACAAATGCAGGAGAAGACAGAAACACAGACTAACATGCCCTTCATGTGATTCTTATGAG
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De Jongh, Karen S.
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Covert, Douglas C.
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Pred. No. 2.6e-91;
0; Mismatches 64
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RESULT 4 US-11-266-748A-401642 ; Sequence 401642, Application US/11266748A

GENERAL INFORMATION:

Publication No. US20060134663A1

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US-11-266-748A-472688/c
US-11-266-748A-472688, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
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US-11-266-748A-401642
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PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
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APPLICANT: Harkin, Paul
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APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology
TITLE OF INVENTION: Methods of Using the Same
FILE REPERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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SOFTWARE: PatentIn version 3
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ORGANISM: Homo
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Similarity 84.1%;
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                                                                                                                                                                             CAGCATCTGTCCTAGAACACACGGAAGTGAAGATTCCTGA
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RESULT 6 US-10-806-611-1

Sequence 1, Application US/10806611
Publication No. US20060159655A1
GENERAL INFORMATION:
APPLICANT: Collins, Mary

APPLICANT: Collins, Mary APPLICANT: Chin, Elaine Y. APPLICANT: Senices, Mayra APPLICANT: Young, Deborah A.

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PRIOR PILING DATE: 2004-11-03
PRIOR PELICATION NUMBER: EP 04105482.6
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
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PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: Patentin version 3.3
SEQ ID NO 472688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 338; Conservative
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (31918)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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ORGANISM: Homo Sapiens
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                           CAGCACCTGTCCTCTCGTACCCCACGGTTCCGAAGATTCCTGA
                                                                                                                    AAAAAACCGCCGAAAGAATTCCTGGAACGTTTCAAATCCCTGCTGCAGAAAATGATTCAC
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CAGCATCTGTCCTCTAGAACACACGGAAGTGAAGATTCCTGA
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                                                                                       AAAAAACCACCCAAAGAATTCCTAGAAAGATTCAAATCACTTCTCCAAAAGATGATTCAT
                                                                                                                                                                           ACAAATGCAGGGAGAAGACAGAAACACAGACTAACATGCCCTTCATGTGATTCTTATGAG
                                                                                                                                                                                                                  ACCAACGCAGGTCGTCAGAAACACCGTCTGACCTGCCCGTCCTGTGATTCTTATGAG
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Pred. No. 2.6e-91;
0; Mismatches 64
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Best Local Similarity 83.8%;
Matches 337; Conservative
                                                                                                                                  NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn versi
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/10806611 Publication No. US20060159655A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 1
Query Match
                                                                                                                                                                                                                                       APPLICANT: Collins, Mary
APPLICANT: Collins, Mary
APPLICANT: Cohin, Elaine Y.
APPLICANT: Senices, Mayra
APPLICANT: Senices, Mayra
APPLICANT: Young, Deborah A.
TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS
TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS
TITLE OF INVENTION: 1015ERLEUKIN-21/ INTERLEUKIN-21 RECEPTOR
FILE REPERENCE: 16158-013001
CURRENT APPLICATION NUMBER: US/10/806,611
CURRENT FILING DATE: 2004-03-22
CURRENT FILING DATE: 2004-03-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS TITLE OF INVENTION: INTERLEUKIN-21/ INTERLEUKIN-21 RECEPTOR FILE REFERENCE: 16158-013001
CURRENT APPLICATION NUMBER: US/10/806,611
CURRENT FILING DATE: 2004-03-22
PRIOR APPLICATION NUMBER: US 60/456,920
PRIOR APPLICATION NUMBER: US 60/456,920
PRIOR FILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/456,920 PRIOR FILING DATE: 2003-03-21
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ORGANISM: Homo sapiens
                                                               LENGTH: 3072
TYPE: DNA
ORGANISM: Mus musculus
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44.9%;
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Pred. No. 8.9e-91;
0; Mismatches 65
Score 182;
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Length 3072;
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APPLICANT: Holderman, Susan D.

TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21

TITLE OF INVENTION: IN A PROKARYOTIC HOST

FILE REFERENCE: 02-12

FULL REFERENCE: 02-12

FULL REFERENCE: 02-12

CURRENT APPLICATION NUMBER: US/10/735,149

CURRENT FILING DATE: 2003-12-12

NUMBER OF SEQ ID NOS: 42

SOOTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 26

LENGTH: 64
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APPLICANT: Chan, Chung
APPLICANT: Zamost, Br
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                                                                                                                                       Matches
                                                                                                                                                     Query Match
Best Local Similarity
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APPLICANT:
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                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
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Covert, Douglas C.
Liu, Hong Y.
De Jongh, Karen S.
                                                                                         TTATAGATATTGTTGATCAGCTGAAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGC 100
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                                 CGGC 104
                                                                   TTATAGATATTGTTGATCAGCTGAAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGC
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 CGGC 64
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Pred. No. 7.2e-12;
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RESULT

GENERAL INFORMATION:

Sequence 25, Application US/10735149 Publication No. US20060134754A1

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APPLICANT: Meyer, Jeffrey D.
APPLICANT: Holderman, Susan D.
TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21
TITLE OF INVENTION: UN A PROKARYOTIC HOST
FILE REFERENCE: 02-12
CURRENT APPLICATION NUMBER: US/10/735,149
CURRENT FILING DATE: 2003-12-12
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 60
TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                           ; FEATURE:
; OTHER INFORMATION: oligonucleotide ZC22965
US-10-735-149-17
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                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Chan, APPLICANT: Zamosi APPLICANT: Coveri APPLICANT: Liu, I APPLICANT: De Jo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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Best Local
                                                     Matches
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APPLICANT:
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APPLICANT: Holderman, Susan D.
TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21
TITLE OF INVENTION: IN A PROKARYOTIC HOST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/735,149
CURRENT FILING DATE: 2003-12-12
NUMBER OF SEQ ID NOS: 42
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APPLICANT: Zamost, Br
APPLICANT: Covert, Dou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 GAG 120
110 AAGATGTTGAGACCAACTGTGAGTGGTCCGCTTTCCCCTGTTTCCCAGAAAGCCCCAGCTGA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 CAGCTGAAAAATTATGTGAATGACCTGGTTCCGGAATTTCCTGCCGGCTCCGGAAGATGTT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 CAGCTGAAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGGCTCCGGAAGATGTT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAG 1
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De Jongh, Karen S.
Meyer, Jeffrey D.
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Covert, Douglas C.
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Covert, Douglas C.
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De Jongh, Karen S.
                                                   Conservative (
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                                                                    14.8%; Score 60;
100.0%; Pred. No.
                                                   0,
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                                                   Mismatches
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                                                                    DB 6; Le
                                                                                  Length 60
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                                                   Indels
                                                   0
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                                                   Gaps
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APPLICANT: Holderman, Susan D.

TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21

TITLE OF INVENTION: IN A PROKARYOTIC HOST

FILE REFERENCE: 02-12

CURRENT APPLICATION NUMBER: US/10/735,149

CURRENT FILING DATE: 2003-12-12

NUMBER OF SEQ ID NOS: 42

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 18

LENGTH: 60

TYPE: DNA

ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                     APPLICANT: Liu, Hong Y.
APPLICANT: De Jongh, Karen S.
APPLICANT: Meyer, Jeffrey D.
APPLICANT: Meyer, Jeffrey D.
APPLICANT: Holderman, Susan D.
TITLE OF INVENTION: VECTORS AND METHODS FOR PROFITING OF INVENTION: IN A PROKARYOTIC HOST FILE REFERENCE: 02-12
CURRENT APPLICATION NUMBER: US/10/735,149
CURRENT FILING DATE: 2003-12-12
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19
LENGTH: 60
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US-10-735-149-18
; Sequence 18, Application US/10735149
; Publication No. US20060134754A1
; GENERAL INFORMATION:
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                                                                                                                                                          ; OTHER INFORMATION: oligonucleotide ZC22967 US-10-735-149-19
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US-10-735-149-19/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Chan, Chung
APPLICANT: Zamost, Bruc
APPLICANT: Covert, Doug
APPLICANT: Liu, Hong Y.
APPLICANT: De Jongh, Ka
APPLICANT: Meyer, Jeffr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19, Application US/10735149
Publication No. US20060134754A1
                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 14.8%; Score 60; DB 6; LA Best Local Similarity 100.0%; Pred. No. 1.6e-10; Matches 60; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Chan, Chung
APPLICANT: Zamost, Br
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                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 AACGAACGTATCAACGTTTCCATTAAAAAACTGAAACGTAAACCGCCGCCGTCCACCAAC 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAACGTAAACCGCCGTCCACCAAC 1
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Covert, Douglas C.
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Covert, Douglas C.
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De Jongh, Karen S.
Meyer, Jeffrey D.
                                                                              Conservative
                                                                                                 14.8%;
100.0%;
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                                                                                               Score 60; DB 6; L
Pred. No. 1.6e-10;
                                                                                Mismatches
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                                                                            Gaps
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RESULT 13 US-10-735-149-20

GENERAL INFORMATION: Sequence 20, Ap Publication No.

Application US/10735149 No. US20060134754A1

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APPLICANT: Chan, Chung
APPLICANT: Zamost, Bruce L.
APPLICANT: Covert, Douglas C.
APPLICANT: Covert, Douglas C.
APPLICANT: De Jongh, Karen S.
APPLICANT: De Jongh, Karen S.
APPLICANT: Meyer, Jeffrey D.
APPLICANT: Meyer, Jeffrey D.
APPLICANT: Molderman, Susan D.
TITLE OF INVENTION: IN A PROKARYOTIC HOST
FILTE REFERENCE: 02-12
CURRENT APPLICATION NUMBER: US/10/735,149
CURRENT FILING DATE: 2003-12-12
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PastSEQ for Windows Version 4.0
I SEQ ID NO 20
I LENGTH: 60
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; OTHER INFORMATION: oligonucleotide ZC22968
US-10-735-149-20
                                                                                                                                                                        ; OTHER INFORMATION: oligonucleotide ZC22969
US-10-735-149-21
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APPLICANT: Chan, Chu
APPLICANT: Zamost, I
APPLICANT: Covert, I
                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/735,149
CURRENT FILING DATE: 2003-12-12
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 60
                                                                                      Matches
                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21, Application US/10735149 Publication No. US20060134754A1
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Best Local Similarity
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APPLICANT: De Jongh, Karen S.

APPLICANT: Meyer, Jeffrey D.

APPLICANT: Holderman, Susan D.

TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21

TITLE OF INVENTION: IN A PROKARYOTIC HOST

FILE REFERENCE: 02-12
                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                         290 GTGATTCTTATGAGAAAAAACCGCCGAAAGAATTCCTGGAACGTTTCAAATCCCTGCTGC 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250 GCAGGTCGTCAGAAACACCGTCTGACCTGCCCGTCCTGTGATTCTTATGAGAAAAAA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60;
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GTGATTCTTATGAGAAAAAACCGCCGAAAGAATTCCTGGAACGTTTCAAATCCCTGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zamost, Bruce L.
Covert, Douglas C.
                                                                                      Conservative
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Conservative 0
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                                                                                                           100.0%;
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                                                                                                           14.8%; Score 60; DB 6; Length 60; 100.0%; Pred. No. 1.6e-10;
                                                                                  0; Mismatches
                                                                                    0;
                                                                                      Indels
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FILE REFERENCE: 02-12
CURRENT APPLICATION NUMBER: US/10/735,149
CURRENT FILING DATE: 2003-12-12
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 60
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                    ; OTHER INFORMATION: oligonucleotide ZC22970 US-10-735-149-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22, Application US/10735149
Publication No. US20066134754A1
GENERAL INFORMATION:
APPLICANT: Chan, Chung
APPLICANT: Zamost, Bruce L.
                                                                            Matches
                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Meyer, Jeffrey D.
APPLICANT: Holderman, Susan D.
TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21
TITLE OF INVENTION: IN A PROKARYOTIC HOST
                  330 ACGTTTCAAATCCCTGCTGCAGAAAATGATTCACCAGCACCTGTCCTCTCGTACCCACGG
                                                                          60;
1 ACGTTTCAAATCCCTGCTGCAGAAAATGATTCACCAGCACCTGTCCTCTCGTACCCACGG 60
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Covert, Douglas C.
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De Jongh, Karen
                                                                            Conservative
                                                                        14.8%; Score 60; DB 6; L
100.0%; Pred. No. 1.6e-10;
tive 0; Mismatches 0;
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                                                                                                                 Length 60
                                                                            Indels
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                                                                            Gaps
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Search completed: August Job time : 1538 secs 7, 2006, 14:03:08

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                             Scoring table:
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Perfect score:
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GenEmbl:*

1: gb_env:
2: gb_pat:
3: gb_pt:
4: gb_pt:
5: gb_pr:
6: gb_rc
7: gb_g
8: gb_g
10: gb
11: gb
11: gb
11: gb
13: gb
14:
                                                                                                                                                                                                                                                                                                           6366136 seqs, 31973710525 residues
                                                                                                                                                                                                                                                                                                                                  Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                  US-10-735-149-27
405
                                                                                                                                                                                                                                                                                                                                                                                                                August 7, 2006, 12:03:42; Search time 2686 Seconds (without alignments) 9642.109 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                     1 atgcaaggtcaagatcgcca.....acggttccgaagattcctga 405
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

18	17	16	15	14	13	12	11	10	9	89	7	σ	υī	4	ω	2	1	Result No.	
299.6	299.6	299.6	299.6	299.6	299.6	299.6	299.6	299.6		299.6	299.6	299.6	299.6	299.6	299.6	299.6	299.6	Score	
74.0	74.0	74.0	74.0	74.0	74.0	74.0	74.0	74.0	•	74.0	74.0	74.0	74.0	74.0	74.0	74.0	74.0	Query Match	P
642	642	642	642	642	642	642	642	642	566	566	566	564	489	483	483	483	483	Query Match Length	
N	N	N	N	N	N	N	N	N	v	σ	σ	σ	N	N	N	N	N	BG	
AR374039	CS237090	CS080568	CS045670	CS043043	CS036718	CS034091	BD248940	AR174547	BC066262	BC066261	BC066258	BC066260	DD180237	AR456247	AR374097	BD248998	AR174605	ID	
AR374039 Sequence	CS237090 Sequence	CS080568 Sequence	CS045670 Sequence	CS043043 Sequence		CS034091 Sequence	BD248940 Novel cyt	AR174547 Sequence	BC066262 Homo sapi	BC066261 Homo sapi	BC066258 Homo sapi	BC066260 Homo sapi	DD180237 Albumin F	AR456247 Sequence	AR374097 Sequence	BD248998 Novel cyt	eque	Description	

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182		_	182	184.2	229.4	231	3 232.2		290.6			3 290.6	293.6		_	_	3 294.8	296	5 296.6		298	N	N		_	_
44.9	44.9	44.9	44.9	45.5	56.6	57.0	57.3	65.3	71.8			71.8	72.5	72.5	72.5	72.5	•	73.2	73.2	73.6	73.6		73.6	•	74.0	74.0
3072	3072	3072	3071	441	459	2801	459	444	486	486	486	486	1560	1560	1560	1560	489	486	486	617	611	566	489	642	642	642
N	N	N	σ	σ	14	14	14	N	N	Ŋ	N	Ŋ	Ŋ	N	N	N	N	Ŋ	N	N	σ	v	N	ហ	N	N
C\$080570	BD248991	AR174598	AF254070	AY428162	AB073020	AB127975	AB073021	AR705418	AR456190	AR374040	BD248941	AR174548	AR456266	AR374116	BD249017	AR174624	AR705419	AX280163	AR577097	DD166615	BC069124	BC066259	CS135974	AF254069	AR705417	AR456189
CS080570 Sequence	BD248991 Novel cyt	AR174598 Sequence	AF254070 Mus muscu	AY428162 Mus muscu	AB073020 Sus scrof	AB127975 Canis fam	AB073021 Bos tauru	AR705418 Sequence	AR456190 Sequence	AR374040 Sequence	BD248941 Novel cyt	AR174548 Sequence	AR456266 Sequence	AR374116 Sequence	BD249017 Novel cyt	AR174624 Sequence	AR705419 Sequence	AX280163 Sequence	AR577097 Sequence	DD166615 Methods a	Homo	BC066259 Homo sapi	CS135974 Sequence	AF254069 Homo sapi		AR456189 Sequence

ALIGNMENTS

dg VQ	d V	Qy Db	Db dd	Quer Best Matcl	SOURCE ORGANIS REFERENCE AUTHORS TITLE JOURNAL FEATURES SOUR	RESULT 1 AR174605 LOCUS DEFINITION ACCESSION VERSION KEYWORDS
184 GGTAACAACGAACGTATCAACGTTTCCATTAAAAAACTGAAACGTAAACCGCCGCCGTCC 243 	124 AACTGTGAGTGGTCCGCTTTTCTCCTGTTTCCAGAAAGCCCAGCTGAAATCCGCAAACACC 183 	64 AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGGCTCCGGAAGATGTTGAGACC 123	4 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 63	Query Match 74.0%; Score 299.6; DB 2; Length 483; Best Local Similarity 84.1%; Pred. No. 3.7e-92; Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;	URCE Unknown. ORGANISM Unknown. Unclassified. Unclassified. I (bases 1 to 483) AUTHORS (FOSS, J. B., Presnell, S.R., Sprecher, C.A., Foster, D.C., Holly, R.D., Gross, J. A., Johnston, J.V., Nelson, A.J., Dillon, S.R. and Hammond, A.K. TITLE (Cytokine zalphall Ligand JOURNAL Patent: US 6307024-A 63 23-OCT-2001; Location/Qualifiers source (organism="unknown" / organism="unknown" / mol_type="unassigned DNA"	RESULT 1 AR174605 AR174605 AR174605 AR174605 DEFINITION Sequence 63 from patent US 6307024. ACCESSION AR174605 VERSION AR174605 KEYWORDS AR174605.1 GI:17914925

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REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
BD248998
LOCUS
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Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                            OS HOMO SEPIENS (human)

PN JP 2002537839-A/59

PD 12-NOV-2002

PF 09-MAR-2000 JP 2000603382

PF 09-MAR-1999 US 09/264908,11-MAR-1999 US

01-JUL-1999 US 60/142013

PI JULIA E NOVAK,SCOTT R PRESNELL,CINDY A SPRECHI
FOSTER,

PI STACEY R DILLON, ANGELA K HAMMOND

PI STACEY R DILLON, ANGELA K HAMMOND

PI C12N15/09, A61K38/00, A61K45/00, A61P35/00, A61P35

PC C07K14/53, C07K14/55, C07K16/24, C07K19/00, C12N1/21,

PC C12N1/21,

PC C12N5/10,C12P21/02,C12P21/02,G01N33/53,C12N15,

A61K37/02

CC NOVEL CYTOKINE ZALPHA11 ligand
FH Key LOCATION/Qualifiers
FT SOURCE 1.483

FT SOURCE (human)
                           142
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                                                                                                                                           338;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent: JP 2002537839-A 59 ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hominidae, Homo.

(bases 1 to 483)

Novak, J.E., Presnell, S.R., Sprecher, C.A., Foster, D.C., Holly, R.D., Gross, J.A., Johnston, J.V., Nelson, A.J., Dillon, S.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BD248998 483 bp
Novel cytokine ZALPHA11 ligand.
BD248998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel cytokine ZALPHA11 ligand
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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AACTGTGAGTGGTCCGCTTTCTCCTGTTTCCAGAAAGCCCAGCTGAAAATCCGCAAACACC 183
                                          AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGGCTCCGGAAGATGTTGAGACC 123
                                                                                                  CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGCATCTGTCCTCTAGAACACACGGAAGTGAAGATTCCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACAAATGCAGGGAGAAGACAGAAACACAGACTAACATGCCCTTCATGTGATTCTTATGAG
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                          AAAAATTATGTGAATGACTTGGTCCCTGAATTTCTGCCAGCTCCAGAAGATGTAGAGACA 201
                                                                                   CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                          RICHARD D HOLLY, JANE A GROSS, JANET V JOHNSTON, ANDREW J NELSON, STACEY R DILLON, ANGELA K HAMMOND C12N15/09, A61K38/00, A61K45/00, A61P35/00, A61P37/00, C07K14/52,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sapiens
                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                      C12N5/10, C12P21/02, C12P21/02, G01N33/53, C12N15/00, C12N5/00,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JULIA E NOVAK, SCOTT R PRESNELL, CINDY A SPRECHER, DONALD
                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                    74.0%;
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                                                                                                                                        Score 299.6; DB 2;
Pred. No. 3.7e-92;
0; Mismatches 64;
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Methods of using zalphall ligand patent: US 6605272-A 63 12-AUG-2003; ZymoGenetics, Inc.; Seattle, WA Location/Qualifiers
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Novak, J.E., Presnell, S.R.,
Gross, J.A., Johnston, J.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hammond, A.K.
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Unclassified.
CAGCACCTGTCCTCGTACCCACGGTTCCGAAGATTCCTGA
                                                                                                                                                                                                                                                                                                                                                                                  AACTGTGAGTGGTCCGCTTTCTCCTGTTTCCAGAAAGCCCCAGCTGAAATCCGGCAAACACC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGGCTCCGGAAGATGTTGAGACC 123
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                                                                                                  AAAAAACCGCCGAAAGAATTCCTGGAACGTTTCAAATCCCTGCTGCAGAAAATGATTCAC 363
                                                                                                                                                                                             ACCAACGCAGGTCGTCAGAAACACCGTCTGACCTGCCCGTCCTGTGATTCTTATGAG
                                                                                                                                                                                                                                                                                         GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAACGTAAACCGCCGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGAAACAATGAAAGGATAATCAATGTATCAATTAAAAAAGCTGAAGAGGAAACCACCTTCC 321
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                                                                        AAAAAACCACCCAAAGAATTCCTAGAAAGATTCAAATCACTTCTCCAAAAAGATGATTCAT 441
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/mol_type="genomic DNA"
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Pred. No. 3.7e-92;
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Hominidae; Homo.
1 (bases 1 to 489)
Haseltine, W.A., Rosen, C.A.,
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Novak, J.E., Presnell, S.R.,
Gross, J.A., Johnston, J.V.,
Hammond, A.K.
                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                          Homo sapiens (human)
Homo sapiens
                                                                                                                                  DD180237.1 GI:83973219
JP 2005514060-A/1222.
                                                                                                                                                                       Albumin Fusion Proteins DD180237
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/mol_type="genomic
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   Ballance, D.
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   Turner, A.J
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Best Local Sim
Matches 338;
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JOURNAL
   ORGANISM
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PN JP 2005514060
PD 19-MAY-2002 1
PF 23-DEC-2002 1
23-DCT-2002 US
18-SEP-2002 US
18-SEP-2002 US
13-AUG-2002 US
05-UNV-2002 US
05-UNV-2002 US
05-UNW-2002 US
21-DEC-2001 US
08-PEB-2002 US
24-PEB-2002 US
24-MAY-2002 US
24-MAY-2002 US
24-MAY-2002 US
15-NOW-2002 US
26-PEB-2002 US
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26-PEB-2002 US
26-PEB-2002 US
27-MAY-2002 US
28-PEB-2002 US
29-PEB-2002 US
29-PEB-2002 US
21-DEC-2001 US
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                                       BC066260
BC066260.1
MGC.
                                                                                            Homo sapiens interleukin IMAGE:6971863), complete
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Patent: JP 2005514060-A 1222 19-MAY-2005;
Human Genome Sciences Inc,Delta Biotechnology Limited,
Pharmaceutical Corporation
                                                                                                                                    BC066260
 Homo sapiens (human)
Homo sapiens
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JP 2005514060-A/1222
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/db_xref="taxon:9606"
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Pred. No. 3.7e-92;
D; Mismatches 64
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REFERENCE
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TITLE
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CE 1 (bases 1 to 564)

Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD, Collins FS, Wagner L, Shemmen CM, Schuler GD, Altschul SF, Zeeberg BB, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T, Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL, Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P, Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH, SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH, Si, Schenzds S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW, Vilalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J, Helton E, Ketteman M, Madan A, Rodriguez S, Sanchez A, Whiting M, Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW, Touchman JW, Green ED, Dickson MC, Rodriguez KO, Grimwood J, Schmutz J, Myers RM, Butterfield YS, Krzywinski MI, Skalska U, Smailus DE, Schmerch A, Schein JE, Jones SJ and Marra MA.

Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 172 Row: d Column: 18
This clone was selected for full length sequencing because it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Director MGC Project.
Direct Submission
Submitted (03-FEB-2004) National Institutes of Health, Mammalian Sene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: Bhat Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db xref="taxon:9606"
/clome="MGC:9378 IMAGE:6971863"
/tissue_type="PCR rescued clones'
/clone_lib="WIH_MGC_195"
/lab_host="DH10B"
                                                                                     /codon_start=1
/product="interleukin 21"
/protein_id="AAH66260.1"
/db_xref="GI:42542588"
                                                                                                                                                                                                                                                                                                      /note="synonyms: Zall,
/db_xref="GeneID:59067"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www-shgc.stanford.edu
(Dickson, Mark) mcd@paxil.stanford.edu
M., Schmutz, J., Grimwood, J., Rodriquez,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eutheria;
                                                                                                                                                                                                             /gene="IL21"
                                                                                                                                                                                                                                                                   /db_xref="MIM:605384"
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                                                                                                                                                                                                                                                                                                                                                                                                                                 note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
                            db_xref="GeneID:59067"
db_xref="MIM:605384"
translation="MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLID
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                                                                                        Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL, Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P, Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Millahy SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunarathe PH, SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunarathe PH, SJ, Bosak SA, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW, Villalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J, Helton E, Ketteman M, Madan A, Rodrigues S, Sanchez A, Whiting M, Helton E, Ketteman M, Madan A, Rodrigues S, Sanchez A, Whiting M, Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW, Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J, Schmutz J, Myers RM, Butterfield YS, Krzywinski MJ, Skalska U, Smallus DE, Schnerch A, Schein JE, Jones SJ and Marra MA.

IM Mammalian Gene Collection Program Team Generation and mouse cDNA semmence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hominidae; Homo.

1 (bases 1 to 566)

Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD, Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD, Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeebe Collins FS, Wagner L, Shenmen CM, Hopkins RF, Jordan H, Moore B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore
                                                      human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94:
Web site:
Web site:
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (03-FEB-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue Procurement: Narayan Bhat
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                                        GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAACGGAAACGTAAACCGCCGTCC
                                                                                                                                                                                                                                                                                                                                                                            AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGGCTCCGGAAGATGTTGAGACC 123
GGAAACAATGAAAGGATAATCAATGTATCAATTAAAAAAGCTGAAGAGGAAACCACCTTCC
                                                                                                                                                 AACTGTGAGTGGTCAGCTTTTTCCTGTTTTTCAGAAGGCCCAACTAAAGTCAGCAAATACA
                                                                                                                                                                                                                          AACTGTGAGTGGTCCGCTTTCTCCTGTTTCCAGAAAGCCCAGCTGAAATCCGCAAACACC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG
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/note="synonyms: Za11, IL-21"
/db_xref="GeneID:59067"
/db_xref="MIM:605384"
46. ..534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="GeneID:59067"
/db_xref="MIM:605384"
/translation="MRSSPGNMERIVICLMVIFLGTLVHKSSSQGDRHMIRWRQLID
/translation="MRSSPGNMERIVICLMVIFLGTLVHKSSSQGDRHMIRWRQLID
/translation="MRSSPGNMERIVICLMVIFLGTLVHKSSSQGDRHMIRWRQLID
/translation="MRSSPGNMERIVICLMVIFLGTLVHKSSSQGDRHMIRWRQLID
/translation="MRSSPGNMERIVICLMVIFLGTLYHIRWRQLID
/translation="MRSSPGNMERIVICL"/"
/tra
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/db_xref="taxon:9606"
/clone="MGC:79376 IMAGE:6971861"
/tissue_type="PCR rescued clones"
/clone_lib="NIH_MGC_195"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="interleukin 21"
/protein_id="AAH66258.1"
/db_xref="GI:42542659"
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/codon_start=1
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84.1%;
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Pred. No. 3.8e-92;
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El (bases 1 to 566)

RS Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD, Strausberg RL, Feingold EA, Grouse LH, Derge JG, Altschul SF, Zeeberg Collins FS, Magner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T, Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL, Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P, Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH, Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW, Villalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J, Helton E, Ketteman M, Madan A, Rodrigues S, Sanchez A, Whiting M, Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW, Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW, Madan A, Sohners BD, Dickson MC, Rodriguez AC, Grimwood J, Schmerch A, Schein JE, Jones SJ and Marra MA.

TM Mammalian Gene Collection Program Team Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             433
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Clone distribution: MGC clone distribution information can be founthrough the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 172 Row: d Column: 16
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 11141874.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Director MGC Project.

Direct Submission

Direct Submission

Submitted (03-FEB-2004) National Institutes of Health, Mammalian Submitted (03-FEB-2004) National Institutes (04-FEB-2004) National 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                    http://www-shgc.stanford.edu
(Dickson, Mark) mcd@paxil.stanford.edu
M., Schmutz, J., Grimwood, J., Rodriquez,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:42542656
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                                                                                                                                                                                         Homo sapiens interleukin IMAGE: 6971866), complete
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                           BC066262
BC066262.1
                                                        Homo sapiens
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ivdolknyvndlupeflpapedvetnoewsafscfgkaolksantgnneriinvsikk
lkrkppstnagrrokhrltcpscdsyekkppkeflerfksllokmihohlssrthgse
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/tissue_type="PCR rescued clones"
/clone_lib="NHH_MGC_195"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="GeneID:59067"
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/db_xref="GeneID:59067"
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/mol_type="mRNA"
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                                                                                                                                           GI:42542806
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Pred. No. 3.8
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RS Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD, Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T, Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL, Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P, Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH, Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW, Villalon DK, Muzny DM, Sodergren EU, Lu X, Gibbs RA, Fahey J, Helton E, Ketteman M, Madan A, Rodrigues S, Sanchez A, Whiting M, Madan A, Young AC, ShevChenko Y, Bouffard GG, Blakeeley RW, Madan A, Young AC, ShevChenko Y, Bouffard GG, Blakeeley RW, Schmutz J, Myers RM, Butterfield YS, Krzywinski MI, Skalska U, Smailus DE, Schmerch A, Schein JE, Jones SJ and Marra MA.

Remaration and initial analyssis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: Capabs remail.nih.gov
Tissue Procurement: Narayan Bhat
Tissue Procurement: Narayan Bhat
CDNA Library Preparation: Bhat Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford,
Genter, Stanford University School of Medicine, Stanford,
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Director MGC Project.

Direct Submission

Submitted (03-FEB-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         passed
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Series: IRAK Plate: 172 Row: d Column: 15
This clone was selected for full length sequencing because
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be for
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 172 Row: d Column: 15
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Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the following selection criteria: matched Location/Qualifiers
                                                                               /product="interleukin 21"
/protein id="AAH66762.1"
/brotein id="AAH66762.1"
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/db_xref="MGmeID:59067"
/db_xref="MIM:605384"
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LKRKPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSE
                                                                                                                                                                                                                                                                                               /note="synonyms: Zall, IL-21"
/db_xref="GeneID:59067"
/db_xref="MIM:605384"
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/clone="MGC:79380 IMAGE:6971866"
/tissue type="PCR rescued clones"
/clone lb="NIH MGC_195"
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                                                                                                                                                                                                                                                     gene="IL21"
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Best Local S
Matches 338
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Best Local Similarity
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                                                                                                                                                                                                                                          1 (bases 1 to 642)
Novak, J.E., Presnell, J.R., Sprecher, C
Gross, J.A., Johnston, J.V., Nelson, A.J
Hammond, A.K.
Cyrokine zalphall Ligand
Patent: US 6307024-A 1 23-OCT-2001;
Location/Qualifiers
22 1. 642
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              AACTGTGAGTGGTCCGCTTTCTCCTGTTTCCAGAAAGCCCAGCTGAAATCCGCAAACACC 183
                                                                 AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGGCTCCGGAAGATGTTGAGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGCACCTGTCCTCGTACCCACGGTTCCGAAGATTCCTGA 405
                                                  AAAAATTATGTGAATGACTTGGTCCCTGAATTTCTGCCAGCTCCAGAAGATGTAGAGACA
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AACTGTGAGTGGTCAGCTTTTTCCTGTTTTCAGAAGGCCCAACTAAAGTCAGCAAATACA
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ilarity 84.1%;
Conservative
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                                                                                                                                                                                                                  /organism="unknown"
/mol_type="unassigned
                                                                                                                                                                                                                                                                                                                                                                                                     GI:17914867
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84.1%;
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Pred. No. 3.8e-92;
0; Mismatches 64;
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                                                                                                                                                                                                                    DNA"
                                                                                                                                                               .6; DB 2;
4e-92;
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Best Local Similarity
Matches 338; Conserv
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PN JP 2002537839-A/1

PD 12-NOV-2002

PF 09-MAR-2000 JP 2000603382

PF 09-MAR-1999 US 09/264908,11-MAR-1999 US 09/265992 PR

01-JUL-1999 US 60/142013

PI JULIA E NOVAK,SCOTT R PRESNELL,CINDY A SPRECHER,DONALD C PI

FOSTER,

PI RICHARD D HOLLY, JANE A GROSS, JANET V JOHNSTON, ANDREW J NELSON,

PI STACEY R DILLON, ANGELA K HAMMOND

PC C12N15/09,A61X38/00,A61X45/00,A61P35/00,A61P37/00,C07K14/52,

PC C07K14/53,

PC C07K14/54,C07K14/55,C07K16/24,C07K19/00,C12N1/15,C12N1/19, PC

C12N1/21,

PC C12N5/10,C12P21/02,C12P21/02,G01N33/53,C12N15/00,C12N5/00, PC

A61K37/02

CC NOVEL Cytokine ZALPHA11 ligand

Location/Qualifiers

(47) . (532).
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64 AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGGCTCCGGAAGATGTTGAGACC 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hominidae; Homo.

1 (bases 1 to 642)

Novak, J.E., Presnell, S.R.,
Gross, J.A., Johnston, J.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Novel cytokine ZALPHA11 ligand.
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                                                                            CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        RICHARD D HOLLY, JANE A GROSS, JANET V JOHNSTON, ANDREW J NELSON STACEY R DILLON, ANGELA K HAMMOND C12N15/09, A61K38/00, A61K45/00, A61P35/00, A61P37/00, C07K14/52, C07K14/53,
                                                                                                                                   Conservative
                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                74.0%;
84.1%;
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                                                                                                                                 Score 299.6; DB Pred. No. 4e-92; 0; Mismatches
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TITLE
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Best Local Similarity
Matches 338; Conserv
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Sequence 3597 from Patent
CS034091 GI:60732828
                                                                                                                                                                                                                                                                                                                                                                                                Patent: WO 2005016962-A 3597 24-FEB-2005
                                                                                                                                                                                                                                                                                                                                                                                                             diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hominidae; Homo.
                                                ACCAACGCAGGTCGTCAGAAACACCGTCTGACCTGCCCGTCCTGTGATTCTTATGAG
                                                                                    GGTAACAACGAACGTATCAACGTTTTCCATTAAAAAACTGAAACGTAAAACCGCCGTCC
                                                                                                                                 AACTGTGAGTGGTCCGCTTTCTCCTGTTTCCAGAAAGCCCCAGCTGAAATCCCGCAAACACC
                                                                                                                                                                    AAAAATTATGTGAATGACTTGGTCCCTGAATTTCTGCCAGCTCCAGAAGATGTAGAGACA
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 AAAAAACCGCCGAAAGAATTCCTGGAACGTTTCAAATCCCTGCTGCAGAAAATGATTCAC
                                                                       GGAAACAATGAAAGGATAATCAATGTATCAATTAAAAAGCTGAAGAGGAAACCACCTTCC
                                                                                                                     AACTGTGAGTGGTCAGCTTTTTCCTGTTTTCAGAAGGCCCAACTAAAGTCAGCAAATACA
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                       ACAAATGCAGGGAGAAGACAGAAACACAGACTAACATGCCCTTCATGTGATTCTTATGAG
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/mol_type="unassigned DNJ
/db_xref="taxon:9606"
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84.1%;
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tch 74.0%; al Similarity 84.1%; 338; Conservative
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Sequence 359
CS043043
CS043043.1
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Sequence 622
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/mol_type="unassigned DN/
/db_xref="taxon:9606"
     GI:61850089
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338; Conserv
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Patent: WO 2005019258-A 3597
                                                            Genentech,
                                                                                      diseases
                                                                                                      Abbas, A., Clark, H., Ouyang, W., Williams, P., Compositions and methods for the treatment
                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                             Homo sapiens
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                                                                         WO 2005019258-A 6224
                                           Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Pred. No. 4e-9
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/db_xref="taxon:9606"

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Search completed: August 7, 2006, 13:58:19
Job time: 2689 secs



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Result
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Maximum
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Perfect score:
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Listing first 45 summaries
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5430.309 Million cell updates/sec
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Adp70484 Codon opt
Aas20695 Fragment
Adh44633 Human Zal
Adi00969 Human zal
Adp19792 Human zal
Adp19792 Human zal
Adw96416 Human zal
Adw41016 Human il.
Adf17040 Human alb
Adv42801 Human alb
Adv42801 Human int
Add17952 Human cDN
Aad47852 Human int
Add100907 Immunity-
Add100907 Immunity-
Add10556 Reference
Adp19730 Human zal
Adp19730 Human int
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290.6	290.6	290.6	291.6	293.6	293.6	293.6	293.6	293.6	293.6	294.8	296.6	296.6	298	298	298	298	298	298	298	298	298	299.6	299.6	299.6	299.6	299.6
71.8	71.8	71.8		72.5	72.5	72.5	72.5	72.5	72.5	72.8	73.2	73.2	73.6	73.6		73.6	73.6		73.6	73.6	73.6	74.0	74.0	74.0	74.0	74.0
486	486	486	642	1560	1560	1560	1560	1560	1560	489	486	399	617	617	617	617	617	617	611	489	489	642	642	642	642	642
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ADH44573	AAS20638	AAA75553	ADY27248	ADV96437	ADP19813	ADI00990	ADH44654	AAS20714	AAA75599	AAD47854	AAD22923	ADW43686	AEG05272	AEE19671	ADS19022	ADJ25620	ACD26729	ACC80873	AEE74873	AEB26427	ADM41018	AED68670	ADZ20500	ADY17791	ADY20418	ADV96354
Adh44573 Degenerat	Aas20638 Degenerat	Aaa75553 Dengenera	Ady27248 Human int	Adv96437 Human zal	Adp19813 Human zal	Adi00990 MBP (malt	Adh44654 Human Zal	Aas20714 DNA encod	Aaa75599 Nucleotid	Aad47854 Human int	Aad22923 Human sol	Adw43686 DNA encod	Aeg05272 Human IL-	Aee19671 Human int	Ads19022 Human int	Adj25620 Human int	Acd26729 cDNA enco	Acc80873 Human IL-	Aee74873 Human IL-	Aeb26427 cDNA enco	Adm41018 Human IL-	Aed68670 Human int	Adz20500 DNA encod	DNA	Ady20418 DNA encod	Adv96354 Human zal

ALIGNMENTS

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RESULT 1
ADP70484
Chang C, Zamost Holderman SD;
                                                                                                                                                                                                            Homo sapiens.
Synthetic.
                                     WPI; 2004-500211/47.
P-PSDB; ADP70485.
                                                                                                 13-DEC-2002; 2002US-0433448P
13-DEC-2002; 2002US-0433452P
                                                                                                                        12-DEC-2003; 2003WO-US039764
                                                                                                                                         01-JUL-2004.
                                                                                                                                                       WO2004055168-A2
                                                                                                                                                                                                                                  interleukin 21; IL-21; human; gene; ss; codon optimised
                                                                                                                                                                                                                                                  Codon optimised interleukin 21
                                                                                                                                                                                                                                                                 23-SEP-2004 (first entry)
                                                                                                                                                                                                                                                                                 ADP70484;
                                                                                                                                                                                                                                                                                               ADP70484 standard; cDNA; 405
                                                                                  (ZYMO ) ZYMOGENETICS INC.
                                                                  BL,
                                                                                                                                                                           /*tag=
                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                     /*tag= a
/product= "interleukin 21 (IL-21)"
                                                                                                                                                                                    . 405
                                                                    Covert
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                                                                                                                                                                                                                                                                                                ₽P
                                                                                                                                                                                                                                                  (IL-21) encoding cDNA SEQ ID
                                                                    Liu HY,
                                                                    De Jongh KS,
                                                                    Meyer JD;
                                                                                                                                                                                                                                                   NO:27
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ADP70458

New expression vectors for the large-scale production of IL-21 proteins comprises a prokaryotic origin of replication, a transcriptional initiation DNA element, a polynucleotide sequence and a transcriptional

terminator.

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RESULT 2
AAS20691
ID AAS2
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XX Prac
XX Natural Arrows
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Best Local
                                                                                                                    Cytokine; zalphall Ligand; zalphall receptor; NK cell progenitor; natural killer cell proliferation; T-cell proliferation; B-cell proliferation; and response; immune system; immunostimulant; cytostatic; human; ss.
                                                                                                                                                                                                                                                                       Fragment of human zalphall Ligand cDNA.
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                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCGGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAACGTAAACCGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCAACTGTGAGTGGTCCGCTTTCTCCTGTTTCCAGAAAGCCCCAGCTGAAATCCGCAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGAAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGGCTCCGGAAGATGTTGAG
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Pred. No. 8.3e-117;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  galphall Ligand and the polynucleotide encoding it. The invention also gives the sequence for the zalphall receptor and the polynucleotide encoding it. The zalphall Ligand polypeptide stimulates proliferation of encoding it. The zalphall Ligand polypeptide stimulates proliferation of NK cells, proliferation of T-cells propertions, the activation of NK cells, proliferation of E-cells stimulated with anti-CD40 antibodies, stimulates an antigenic response in a mammal, and reduces proliferation of E-cells stimulated with anti-IgM antibodies. The zalphall Ligand polypeptide is also useful in preparing antibodies that bind to zalphall Ligand epitopes. The zalphall Ligand polypuncleotides can be used as probes or primers to clone regions of a zalphall Ligand gene, and in gene therapy. Zalphall ligand may also be used to identify inhibitors of its activity, to enhance the generation of anti-tumour responses with or without the infusion of donor lymphocytes, and to activate or stimulate the immune system. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New zalphall ligand polypeptides and polynucleotides, useful for stimulating proliferation, activation, differentiation and/or induction of inhibition of specialized cell function, or for stimulating an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-MAR-1999;
11-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fragment of human zalphall Ligand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                        AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGGCTCCGGAAGATGTTGAGACC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG
                                                                                                                                                            ACCAACGCAGGTCGTCGTCAGAAACACCGTCTGACCTGCCCGTCCTGTGATTCTTATGAG
                                                                                                                                                                                                                                  GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAACGTAAACCGCCGTCC
CAGCATCTGTCCTCTAGAACACACGGAAGTGAAGATTCCTGA
                      CAGCACCTGTCCTCGTACCCACGGTTCCGAAGATTCCTGA
                                                                AAAAAACCACCCAAAGAATTCCTAGAAAGATTCAAATCACTTCTCCAAAAGATGATTCAT 441
                                                                                            AAAAAACCGCCGAAAGAATTCCTGGAACGTTTCAAATCCCTGCTGCAGAAAATGATTCAC 363
                                                                                                                                        ACAAATGCAGGGAGAAGACAGAAACACAGACTAACATGCCCTTCATGTGATTCTTATGAG
                                                                                                                                                                                                            GCAAACAATGAAAGGATAATCAATGTATCAATTAAAAAAGCTGAAGAGGAAACCACCTTCC
                                                                                                                                                                                                                                                                                    AACTGTGAGTGGTCAGCTTTTTCCTGTTTTCAGAAGGCCCAACTAAAGTCAGCAAATACA
                                                                                                                                                                                                                                                                                                                     AACTGTGAGTGGTCCGCTTTCTCCTGTTTCCAGAAAGCCCAGCTGAAATCCGCAAACACC 183
                                                                                                                                                                                                                                                                                                                                                        AAAAATTATGTGAATGACTTGGTCCCTGAATTTCTGCCAGCTCCAGAAGATGTAGAGACA
                                                                                                                                                                                                                                                                                                                                                                                                                          CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG
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Johnston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Col 151-152; 105pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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99US-0123904P.
99US-0142013P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74.0%;
84.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           relates to the isolation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sprecher CA, Foster DO Nelson AJ, Dillon SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 1.3e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 299.6; DB 6
Pred. No. 1.3e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a novel cytokine,
t. The invention a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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ALBULT 3
ADH44633
ID ADH4
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                                                                                                                       The invention relates to stimulating an immune response in a mammal CC exposed to an antigen or pathogen comprises administering a composition CC comprising mature zalphall ligand polypeptide comprising residues 32-162 CC of ADH44572 in a pharmaceutical vehicle. Also included are stimulating an CC (comprising: (a) determining (in)directly the level of antigen or pathogen CC (comprising (in)directly the level of antigen or pathogen present in the mammal; (b) administering a composition CC comprising zalphall ligand polypeptide in a pharmaceutical vehicle; (c) CC determining (in)directly the level of antigen or pathogen in the mammal; (c) and (d) comparing the antigen or pathogen for pathogen in the mammal; (c) change in the level indicates stimulation of immune response), and CC thange in the level indicates stimulation of immune response), and CC spathogen (comprising; (a) determining a level of antigen or pathogen-comprising; (a) determining a level of an antigen or pathogen (comprising; (a) determining a level of antigen or pathogen-comprising a post CC dipper stimulation level of the antigen- or pathogen-specific antibody; (b) administering a composition comprising zalphall CC ligand polypeptide in a pharmaceutical vehicle; (c) determining a post CC (d) comparing the level of the antibody in (a) with (b), where an CC increase in the antibody level indicates stimulation of immune response). CC The method is useful for stimulating an immune response in a mammal CC exposed to an antigen or pathogen, and for enhancing anti-tumour activity resulting in a reduction in tumour progression, decrease in metastasis, CC or tumour stasis, The tumour may be a haematopoietic tumour, a lymphoma CC range of diseases arising from defects in the immune system, e.g. CC systemic lupus servthematosus, rheumatoid arthritis. mysthemia gravis. Or systemic lupus erythematosus, rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novak JE,
Gross JA,
systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis, diabetes, for boosting immunity to infectious diseases, treating immunocompromised parients, such as HTV+ parients and in improving vaccines. The present sequence is a human Zalphall ligand cDNA (or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stimulating an immune response in a mammal exposed to an antigen or pathogen, useful for enhancing anti-tumor activity resulting in reduced tumor progression or metastasis, comprises administering zalphall ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 25; SEQ ID NO 63; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-895283/82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-MAR-2000;
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01-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Zalphall ligand cDNA fragment.
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Johnston
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Nelson AJ,
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J, Dillon SR,
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Best Local :
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                                                             New zalphall ligand polypeptides, infectious diseases, and treating human immunodeficiency virus (HIV)
                       Example
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Johnston
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                     NO 63; 113pp;
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                                                                                                                                                                                                     Sprecher CA, Foster DC,
Nelson AJ, Dillon SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infectious disease; immunocompromised patient;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 299.6;
Pred. No. 1.
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                       English
                                                               useful for boosting immunity immunocompromised patients, s') patients, or in improving va
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID
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                                                                 improving vaccines
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                                                                                                                                                            09-MAR-1999;
11-MAR-1999;
01-JUL-1999;
09-MAR-2000;
                           Novak JE,
Gross JA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic; zalphall ligand; pharmaceutical; cancer; immune response; melanoma; tumour; solid tumour; haematopoietic tumour; lymphoma; huma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human zalphall ligand fragment seqid 63
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                                                                                                          OMYZ)
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                                                                                                          ) ZYMOGENETICS INC
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                           Sprecher CA,
Nelson AJ, 1
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Pred. No. 1.3e-83;
                         , Foster DC,
Dillon SR, 1
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                           , Holly
Hammond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG
                       CAGCACCTGTCCTCCGTACCCACGGTTCCGAAGATTCCTGA 405
                                                                                               AAAAAACCGCCGAAAGAATTCCTGGAACGTTTCAAATCCCTGCTGCAGAAAATGATTCAC
                                                                                                                                                                           ACCAACGCAGGTCGTCGTCAGAAACACCGTCTGACCTGCCCGTCCTGTGATTCTTATGAG
                                                                                                                                                                                                                                                                                                        AACTGTGAGTGAGCTTTTTCCTGTTTTTCAGAAGGCCCAACTAAAGTCAGCAAATACA
                                                                                                                                                                                                                                                                                                                                              AACTGTGAGTGGTCCGCTTTCTCCTGTTTCCAGAAAGCCCAGCTGAAATCCCGCAAACACC
                                                                                                                                                                                                                                                                                                                                                                                    AAAATTATGTGAATGACTTGGTCCCTGAATTTCTGCCAGCTCCAGAAGATGTAGAGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG
CAGCATCTGTCCTCTAGAACACACGGAAGTGAAGATTCCTGA
                                                                         AAAAAACCACCCAAAGAATTCCTAGAAAGATTCAAATCACTTCTCCAAAAGATGATTCAT
                                                                                                                                                   ACAAATGCAGGGAGAAGACAGAAACACAGACTAACATGCCCTTCATGTGATTCTTATGAG
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                                                                                                                                                                                                                                                                GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAACGTAAACCGCCGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP; 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.0%;
84.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; 96 G; 117 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 299.6;
Pred. No. 1.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .3e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
483
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                                                                           441
                                                                                                                                                     381
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Best Local (
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                                                                                                                                                                                                                                                                  The invention comprises a fusion protein that contains a zalphall ligand and a cytokine polypeptide (e.g. IL-2, IL-4, IL-15 or GM-CSF), the fusion protein of the invention binds to the annual receptor protein. The protein of the invention is useful for stimulating the proliferation and/or development of hematopoletic cells. The protein of the invention is also useful in autologous marrow culture. The present cDNA sequence represents a fragment of the human zalphall ligand coding sequence.
                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                       Example
                                                                                                                                                                                                                                                                                                                                                                                    New zalpha 11 Ligand fusion protein, useful for stimulating proliferation and/or development of hematopoietic cells in v
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NELS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SPRE/)
(FOST/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1999;
09-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-MAR-1999;
11-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-2004;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NOVA/)
                                                                                                                                                                                                                                                                                                                                                                                                                    2005-038783/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell; cell
                  244
                                                                                                                        142
322
                                                           184
                                                                               202
                                                                                                    124
                                                                                                                                                                                                                                                                                                                                                                                                                                        JA,
                                                                                                                                           64
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                                                                                                                                                                                    4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRESNELL S R.
SPRECHER C A.
SPRECHER D C.
HOLLY R D.
GROSS J A.
JOHNSTON J V.
NELSON A J.
DILLON S R.
                                                                                                                                                                                                                    Similarity
                                                                                            AACTGTGAGTGGTCCGCTTTTCTCCTGTTTTCCAGAAAGCCCCAGCTGAAATCCCGCAAACACC
                                                                                                                                                                                                                                                 483
ACAAATGCAGGGAGAAGACAGAAACACAGACTAACATGCCCTTCATGTGATTCTTATGAG
            ACCAACGCAGGTCGTCGTCAGAAACACCGTCTGACCTGCCCGTCCTGTGATTCTTATGAG
                                      GGAAACAATGAAAGGATAATCAATGTATCAATTAAAAAAGCTGAAGAGGAAACCACCTTCC
                                                     GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAACGTAAACCGCCGTCC
                                                                                                                                            AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGGCTCCGGAAGATGTTGAGACC
                                                                                                                                                                                     CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG
                                                                                                                                                                                                                                                                                                                                                                            ij
                                                                                                                                                                                                                                                                                                                                                                                                                                         Johnston
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Presnell
                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                        SEQ ID
                                                                                                                                                                                                                                                 BP;
                                                                                                                                                                                                                                                                                                                                                                           autologous marrow culture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2004US-00787442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-00522217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0123547P.
99US-0123904P.
99US-0142013P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            culture; zalphall ligand; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                         SR,
                                                                                                                                                                                                                   74.0%;
84.1%;
                                                                                                                                                                                                                                                A; 103
                                                                                                                                                                                                                                                                                                                                                      63; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sprecher CA,
Nelson AJ, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence -
                                                                                                                                                                                                        0,
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                                                                                                                                                                                                                   Score 299.6;
Pred. No. 1.3
                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Foster DC,
                                                                                                                                                                                                                    .3e-83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        SR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Hammond
                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                      in vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                        AK;
                                                                                                                                                                                                        <u>,</u>
                                                                                                                                                                                                                                                                                                                         the fusion
                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                protein
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381
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8 B

64

AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGGCTCCGGAAGATGTTGAGACC

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                                    Query Match
Best Local S
Matches 338
                                                                                                                                                                                                                                                                                                                                                                                                                                   11-OCT-2002;
16-OCT-2002;
17-OCT-2002;
                                                                                                                          treatment of diseases or conditions where eosinophils are involved in a protective response in a subject, e.g. allergic conditions and/or parasitic diseases. Methods of the invention are useful for the treatment of diseases or conditions where eosinophils are involved in a protective response in a subject, such as allergic conditions (e.g. asthma, allergic rhinitis or allergic diseases of the skin) and/or parasitic diseases, especially helminthic infection. The current sequence represents the DNA sequence encoding IL-21. Note: This sequence does not decode to that of ADM41017, which we are told in the specification is the amino acid
                                                                                                                                                                                                                                                                                                Use of Interleukin-21 for the treatment of diseases or conditions eosinophils are involved in a protective response in a subject, e. allergic conditions and/or parasitic diseases.
                                                                                        Sequence
                                                                                                                                                                                                                                                The invention relates to
                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 1; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anthelmintic; dermato eosinophil; allergic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADM41016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-OCT-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2004032953-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antiallergic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADM41016;
                                                                                                                                                                                                                                                                                                                                                                                                          (NOVO ) NOVO NORDISK
                                      338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IL-21
                                                  Similarity
                                                                                        488
CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGCACCTGTCCTCGTACCCCACGGTTCCGAAGATTCCTGA
                                                                                                                  of IL-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGCATCTGTCCTAGAACACACGGAAGTGAAGATTCCTGA 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAAAACCACCCAAAGAATTCCTAGAAAGATTCAAATCACTTCTCCAAAAGATGATTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAAAACCGCCGAAAGAATTCCTGGAACGTTTCAAATCCCTGCTGCAGAAAATGATTCAC
                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                   2002DK-00001587.
2002DK-00001587.
2002US-0419225P.
                                                                                        BP; 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2003WO-DK000691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiasthmatic; antiparasitic; antiinflammatory;
dermatological; immunomodulator; interleukin; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry
                                                74.0%;
84.1%;
                                                                                       A; 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              parasitic; asthma; allergic rhinitis;
gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           488
                                                                                                                                                                                                                                                  an interleukin (IL)-21 that is used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              geq
                                   ; Score 299.6; [
; Pred. No. 1.3e-
0; Mismatches
                                                                                       C; 98 G; 117 T; 0 U; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              id
                                               299.6; DB 1
No. 1.3e-83;
                                                              DB 12;
                                       64;
                                       Indels
                                                              Length
                                                                                         Other;
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                                                                 488;
                                      0,
                                       Gaps
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              63
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                                                                                           21-DEC-2001;
24-JAN-2002;
28-JAN-2002;
26-FEB-2002;
26-FEB-2002;
27-MAR-2002;
27-MAR-2002;
21-MAY-2002;
24-MAY-2002;
24-MAY-2002;
24-MAY-2002;
25-UN-2002;
205-JUN-2002;
10-JUL-2002;
10-JUL-2002;
11-AUG-2002;
11-AUG-2002;
11-AUG-2002;
11-AUG-2002;
11-SEP-2002;
11-SEP-2002;
11-SEP-2002;
11-CCT-2002;
11-CCT-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                           serum osmotic pressure; shelf-life; stability; ar gene therapy; diabetes mellitus; human; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       albumin fusion protein; albumin activity; human serum albumin; serum osmotic pressure; shelf-life; stability; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                23-DEC-2002; 2002WO-US040891
                                                                                                                                                                                                                                                                                                                                                                        24-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human albumin fusion protein-related DNA sequence SeqID2157.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-FEB-2004
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            Ballance
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                                HUMAN GENOME SCI INC.
DELTA BIOTECHNOLOGY I
PRINCIPIA PHARM CORP.
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12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGCACCTGTCCTCGTACCCACGGTTCCGAAGATTCCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAAAACCGCCGAAAGAATTCCTGGAACGTTTCAAATCCCTGCTGCAGAAAATGATTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAACGTAAACCGCCGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGCATCTGTCCTCTAGAACACACGGAAGTGAAGATTCCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAAAACCACCCAAAGAATTCCTAGAAAGATTCAAATCACTTCTCCAAAAGATGATTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACAAATGCAGGAGAAGACAGAAACACAGACTAACATGCCCTTCATGTGATTCTTATGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCAACGCAGGTCGTCAGAAACACCGTCTGACCTGCCCGTCCTGTGATTCTTATGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AACTGTGAGTGGTCAGCTTTTTCCTGTTTTCAGAAGGCCCAACTAAAGTCAGCAAATACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACTGTGAGTGGTCCGCTTTCTCCTGTTTCCAGAAAGCCCAGCTGAAATCCGCAAACACC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAAATTATGTGAATGACTTGGTCCCTGAATTTCTGCCAGCTCCAGAAGATGTAGAGACA 206
                                                                               2001US-0341811P.
2002US-0351360P.
2002US-0351360P.
2002US-0359370P.
2002US-0367500P.
2002US-0367500P.
2002US-038750P.
2002US-0382617P.
2002US-0382617P.
2002US-0383123P.
2002US-0385708P.
2002US-0385708P.
2002US-0398008P.
2002US-0402131P.
2002US-0402131P.
2002US-0411356P.
2002US-0411356P.
2002US-0411364P.
2002US-041761P.
2002US-041761P.
2002US-0420246P.
2002US-0423623P.
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           Turner
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           Rosen
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           Haseltine
           WA;
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Matches 338; Query Match Best Local :

Conservative

0; Mismatches Score 299.6; Pred. No. 1.

Indels Length

<u>.</u>.

Gaps

0

489;

1.3e-83; DB 64; 10;

Local Similarity

74.0%; 84.1%;

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This invention relates to a novel albumin fusion protein having albumin CC or biological activity. Human serum albumin is responsible for a CC significant proportion of the osmotic pressure of serum and also CC functions as a carrier of endogenous and exogenous ligands. The fusion of CC functions as a carrier of endogenous and exogenous ligands. The fusion of CC the therapeutic protein. The albumin fusion protein of the invention may CC albumin for compositions with antidiabetic activity whilst the CC nucleotide sequence which encodes it may be useful for gene therapy. The CC albumin fusion protein is useful for preparing a composition for treating CC diabetes mellitus. The present sequence is a DNA sequence which encodes a CC therapeutic protein of the invention. Note: The sequence data for this CC patent did not form part of the printed specification, but was obtained CC in electronic format directly from WIDO at
Sequence 489 BP; 170 A; 103 C; 98 G; 118 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-598517/56.
P-PSDB; ADF17046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; SEQ ID NO 2157; 24pp; English.
                                              ftp.wipo.int/pub/publishedpct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  albumin fusion protein, useful for preparing a composition for aring diabetes mellitus.
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                CAGCACCTGTCCTCTCGTACCCCACGGTTCCGAAGATTCCTGA
                                                                      AAAAAACCGCCGAAAGAATTCCTGGAACGTTTCAAATCCCTGCTGCAGAAAATGATTCAC
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           microarray; psychoneuroendocrinimmune; chronic fatigue; non-insulin dependent diabetes; allergy; immune disorde cancer; neoplasm; infection; expressed sequence tag; ss
                                                                                                  10-MAR-2005
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                                                                    psychoneuroendocrinimmune expressed sequence tag
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a new microarray which comprises probes genes involved in psychoneuroendocrinimmune (PNI) activity. The microarray is useful in diagnosing a condition associated with PNI activity, such as CFS, type-2 diabetes, allergic condition, inflau cancer and infection. The present sequence represents a psychoneuroendocrinimmune gene expressed sequence tag. Note the specificatio mentions SEQ ID NO of up to 3314 but only sequences SEQ ID NO 1829 are provided.
                                    AAA75552 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New microarray comprising psychoneuroendocrinimmune condition associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nicholson A,
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Similarity 84.1%;
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Pred. No. 1.3
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11-MAR-1999;
01-JUL-1999;
                                                                                                                                                                                                                                                                                   proliferation and development of haematopoietic cells in vitro and in vivo. Zalphall ligand polynucleotides can be used as primers or probes for cloning the zalphall gene. The zalphall ligand is useful for treating tumourigenesis. A zalphall ligand-saporin fusion toxin may be used for treating leukaemias and lymphomas. Antagonists against zalphall ligand are useful as research reagents for characterizing ligand-receptor interaction. Antagonists are also useful for inhibiting expansion, proliferation, activation and differentiation of cells involved in regulating hematopoiesis. The zalphall ligand may also be used to stimulate an immune response against B cell tumour, a virus, a parasite or a bacterium. The zalphall polypeptides, polymucleotides, antagonists, agonists and antibodies are also useful for the detection, diagnosis, prevention, and treatment of diseases associated with a zalphall ligand
                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human cytokine, designated zalphall ligand, useful for stimulating the proliferation and/or development of hematopoietic cells in vitro and in vivo, and for treating tumorigenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes a human zalphall ligand polypeptide, whis a cytokine. The zalphall ligand is useful for stimulating the proliferation and development of haematopoietic cells in vitro and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 14; Page 204-205; 256pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     zalphall ligand; cytokine; haematopoietic cell proliferation; tumourigenesis; leukaemia; hematopoiesis; B cell tumour; ss.
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                                                          AAAAATTATGTGAATGACTTGGTCCCTGAATTTCTGCCAGCTCCAGAAGATGTAGAGACA
               AACTGTGAGTGGTCCGCTTTCTCCTGTTTTCCAGAAAGCCCAGCTGAAATCCGCAAACACC 183
                                                                             AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGGCTCCGGAAGATGTTGAGACC
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99US-00265992.
99US-0142013P.
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84.1%;
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Nelson AJ,
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                                                                                                                                                                              Score 299.6; DB 3
Pred. No. 1.5e-83;
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11-MAR-1999;
01-JUL-1999;
The present invention relates to the isolation of a novel cytokine, zalphall Ligand and the polymucleotide encoding it. The invention a gives the sequence for the zalphall receptor and the polymucleotide encoding it. The zalphall Ligand polypeptide stimulates proliferation
                                                                                                                                                                                                                                                                                                              New zalphall ligand polypeptides and polynucleotides, useful for stimulating proliferation, activation, differentiation and/or induction of inhibition of specialized cell function, or for stimulating an
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DB; AAU11965.
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Johnston JV,
                                                                                                                                                                                                        င္ပ
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99US-0123904P.
99US-0142013P.
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140 .532
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systemic lupus erythematosus; zalphall ligand; ds.

sapiens

Location/Qualifiers /product= "IL-21"

/*tag=

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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                   Interleukin-21; IL-2:
autoimmune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human interleukin-21 (IL-21) DNA.
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                                                                                                                                                                                                                                                                                                                 IL-21; antagonist; cancer; inflammatory;
rder; rheumatoid arthritis; multiple sclerosis;
erythematosus; myasthenia gravis; diabetes; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74.0%;
84.1%;
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Pred. No. 1.5e-83;
0; Mismatches 64
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to polynucleotides and polypeptides of interleukin-21 (II-21) antagonists, that bind with specificity and exhibit an EC50 that is not detectable in receptor binding studies. The antagonists of the invention have mutations in the D helix of the II-21 molecule, and can be used to inhibit the activity of II-21 with its cognate receptor. The II-21 antagonists are useful for diagnosing and treating disorders involving the aberrant expression or activity of the II-21 polypeptide, such as cancer, inflammatory and autoimmune disorders, including rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus, myasthenia gravis and diabetes. The polypeptides can also be used to prepare antibodies that bind II-21 epitopes, peptides or polypeptides, and for enhancing in vivo killing of target tissues. The present sequence is human II-21 (originally designated zalphall ligand) DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New IL-21 polypeptide and encoding polynucleotide, useful for diagnosing and treating disorders with aberrant expression or activity of the IL-21 polypeptide, such as cancer, rheumatoid arthritis, multiple sclerosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 52-53; 71pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Presnell SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-OCT-2002;
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)B; AAE14932.
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                                                                                                                                                                                                                                                   ACCAACGCAGGTCGTCAGAAAACACCGTCTGACCTGCCCGTCCTGTGATTCTTATGAG
                                                                                                                                                                                                                                                                                                                  GGTAACAACGAACGTATCAACGTTTCCATTAAAAAACTGAAACGTAAACCGCCGTCC
                                                                                                                                                                                                                                                                                                                                                                                   AACTGTGAGTGGTCCGCTTTCCCCTGTTTCCAGAAAGCCCAGCTGAAATCCGGCAAACACCC
                                                                                                                                                                                                                                                                                                                                                                                                                              AAAAATTATGTGAATGACTTGGTCCCTGAATTTCTGCCAGCTCCAGAAGATGTAGAGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG
                                                                                                                              CAGCACCIGICCTCCCTACCCACGGITCCGAAGATTCCTGA 405
                                                                                                                                                                                                                                                                                                                                                               AACTGTGAGTGGTCAGCTTTTTCCTGTTTTCAGAAGGCCCAACTAAAGTCAGCAAATACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAAATTATGTGAATGACCTGGTTCCGGAATTCCCTGCCGGCTCCGGAAGATGTTGAGACC
                                                                                                                                                                                                                                                                                               GGAAACAATGAAAGGATAATCAATGTATCAATTAAAAAAGCTGAAGAGGAAACCACCTTCC
                                                                                                                                                                                                                                ACAAATGCAGGGAGAAGACAGAAACACAGACTAACATGCCCTTCATGTGATTCTTATGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 A; 127 C; 129 G; 166 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74.0%;
84.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 299.6; DB 9;
Pred. No. 1.5e-83;
0; Mismatches 64;
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ADH44571 standard; cDNA;

642 BP

Query Match Best Local Similarity

74.0%; 84.1%; A; 127

Score 299.6; Pred. No. 1.

DB 10; T; 0 U;

220

C; 129

G; 166

0 Other; Length 642;

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CC immune response in a mammal exposed to an antigen or pathogen (c) determining (in) directly the level of antigen or pathogen (c) pathogen present in the mammal; (b) administering a composition (c) determining (in)directly the level of antigen or pathogen in the mammal; (c) and (d) comparing the antigen or pathogen in the mammal; (c) and (d) comparing the antigen or pathogen antigen or pathogen in the mammal; (c) and (d) comparing the antigen or pathogen in the mammal; (e) antigen or pathogen in the mammal; (in) determining a level in (a) with (b), where a cc change in the level indicates stimulation of immune response), and (d) comparing; (e) determining a level of antigen or pathogen or pathogen; (b) administering a composition comprising zalphall (c) igand polypeptide in a pharmaceutical vehicle; (c) determining a post administration level of the antibody in (a) with (b), where an comparing the level of the antibody in (a) with (b), where an comparing the level of the antibody in (a) with (b), where an comparing the level of the antibody in (a) with (b), where an cc mammal in the method is useful for stimulating an immune response in a mammal composed to an antigen or pathogen, and for enhancing anti-tumour activity resulting in a reduction in tumour progression, decrease in metastasis, or tumour stasis. The tumour may be a haematopoletic tumour, a lymphoma or a cell tumour because in the immune system, e.g. c systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis, or diabetes, for boosting immunity to infectious diseases, treating community to infectious diseases, treating constants. The present sequence is a human Zalphall ligand constants and in improving constants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to stimulating an immune response in a mammal exposed to an antigen or pathogen comprises administering a composition comprising mature zalphall ligand polypeptide comprising residues 32-162 of ADH44572 in a pharmaceutical vehicle. Also included are stimulating are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stimulating an immune response in a mammal exposed to an antigen or pathogen, useful for enhancing anti-tumor activity resulting in reduced tumor progression or metastasis, comprises administering zalphall ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 7; SEQ ID NO 1; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-895283/82
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11-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; ss; Zalphall ligand; Zalphall receptor; immune response; tumour progression; metastasis; tumour stasis; haematopoietic tumour; tumour progression; metastasis; tumour stasis; haematosus; lymphoma; B cell tumour; systemic lupus erythematosus; rheumatoid arthritis; myasthenia gravis; diabetes; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-AUG-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; 99US-0123547P.
; 99US-0123904P.
; 99US-0142013P.
; 2000US-00522217.
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Nelson AJ, Dillon SR,
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RESULT 14
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The invention relates to a novel isolated zalphall ligand polypeptide. The polypeptide of the invention may be useful for boosting immunity to infectious diseases and treating immunocompromised patients, such as HIV patients, as well as in improving vaccines. The current sequence is that of the human zalphall ligand cDNA of the invention.
                                                                                                                                                                                                                    New zalphall ligand polypeptides, useful for boosting immunity to infectious diseases, and treating immunocompromised patients, such as human immunodeficiency virus (HIV) patients, or in improving vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                zalphall ligand; immunity; infectious disease;
HIV; vaccine; human; ss; gene.
                                                                                                                                                                    Claim 19; SEQ ID NO 1; 113pp; English.
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DB; ADI00908.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Sprecher CA, Foster DC, Nelson AJ, Dillon SR, 1
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        RESULT 15
ADH10500
ID ADH107500
AC ADH10
XX IL-21
KW IL-21
KW Hepat
KW Antib
XX Homo
X
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Query Match
Best Local Similarity
Matches 338; Conserv
                                                                                                                                                                                           06-JUN-2003; 2003WO-US017808
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Treating Non-Hodgkin's lymphoma,
                                                                                                                                                         07-JUN-2002; 2002US-0387127P
                                                                                                                                                                                                                            18-DEC-2003
                                                                                                                                                                                                                                                                WO2003103589-A2
                                                                                                                                                                                                                                                                                                                                                                                                                        antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      IL-21; interleukin-21; cytostatic; virucide; antiinflammatory;
                                                    2004-062206/06
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                                                                                                                                                                                                                                                                                                                                                                                                                    neuroprotective; muscular; respiratory; antiarthritic;
; anti-HIV; gene therapy; cancer; human; gene; ds.
                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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/product= "interleukin-21'
                                                                                                                                                                                                                                                                                                                    /*tag=
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0; Mismatches 64
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Pred. No. 1.5
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                                                                                      RD,
   cancer or infection comprises
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                                                                                    Kindsvogel
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The invention relates to treating Non-Hodgkin's lymphoma, cancer or CC infection and involves administering to the subject a polypeptide having CC a functional activity of interleukin-21 (IL-21). The methods are useful CC for treating Non-Hodgkin's lymphoma; cancer such as renal cell carcinoma, cepithelial carcinoma, breast cancer, prostate cancer, ovarian cancer and CC colon cancer; viral infection such as AIDS, Hegatitis B or C virus, CC gastroenteritis, haemorrhagic diseases, enteritis, carditis, carditis, paralysis, brochiolitis, upper or lower respiratory CC encephalitis, paralysis, brochiolitis, upper or lower respiratory CC disease, respiratory papillomatosis, arthritis, disseminated disease, CC meningitis, and mononucleosis; or bacterial infection, such as an CC infection by a bacteria selected from chlamydiae, listeriae, helicobacter CC pylori, mycobacteria selected from chlamydiae, listeriae, helicobacter CC curuses, Epstein-Barr virus, Cytomegalovirus, Pox viruses Simplex CY viruses, Pastein-Barr virus, Orthomyzoviruses, Paramyzoviruses, CC Influenza viruses, caliciviruses, rabies viruses, and rinderpest viruses. CC The present sequence represents a DNA encoding a human IL-21 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 642 BP; 220 A; 127 C; 129 G; 166 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 1; 154pp; English.
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                                 364 CAGCACCTGTCCTCTCGTACCCCACGGTTCCGAAGATTCCTGA 405
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338; Conserv
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                                                                                                                                                       AAAAAACCGCCGAAAGAATTCCTGGAACGTTTCAAATCCCTGCTGCAGAAAATGATTCAC
                                                                                                                                                                                                                                                                                  ACCAACGCAGGTCGTCGTCAGAAACACCGTCTGACCTGCCCGTCCTGTGATTCTTATGAG
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CAGCATCTGTCCTCTAGAACACACGGAAGTGAAGATTCCTGA 535
                                                                                                                  AAAAAACCACCCAAAGAATTCCTAGAAAGATTCAAATCACTTCTCCAAAAGATGATTCAT
                                                                                                                                                                                                                                       ACAAATGCAGGGAGAAGACAGAAACACAGACTAACATGCCCTTCATGTGATTCTTATGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACTGTGAGTGGTCAGCTTTTTCCTGTTTTCAGAAGGCCCAACTAAAGTCAGCAAATACA
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84.1%; Pred. No. 1.5
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ALIGNMENTS

JOURNAL PUBMED REFERENCE AUTHORS REFERENCE AUTHORS ACCESSION VERSION KEYWORDS RESULT 1 AY417615 LOCUS ORIGIN FEATURES COMMENT SOURCE DEFINITION TITLE JOURNAL TITLE ORGANISM gene source Hominidae; Homo.

1 (bases 1 to 489)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, J.
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, J.
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Science 302 (5652), 1960-1963 (2003) 14671302 AY417615

Homo sapiens IL21 gene, VIRTUAL gene trios Homo sapiens (human) AY417615.1 GI:39773575 genomic survey sequence AY417615 sequence was made by sequencing genomic exons and ordering based on alignment. /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" Location/Qualifiers /gene="IL21" locus_tag="HCM6283" TRANSCRIPT, DNA linear GSS 17-DEC-2003, partial sequence, Kejariwal, A.,

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                       Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                    found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: IRBK2 row: g column: 10
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information ca
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/clone="IMAGB:6971867"
/tissue_type="mixed"
/lab_host="DH5A_(Tl_phage-resistant)"
/clone_lib="NIH_MGC_195"
                                                                               organism="Homo sapiens'
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                           Location/Qualifiers
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Pred. No. 9.5e-83;
0; Mismatches 64;
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                                          CAGCACCTGTCCTCGTACCCACGGTTCCGAAGATTCCTGA 405
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CAGCATCTGTCCTCTAGAACACACGGAAGTGAAGATTCCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/fearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."
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0; Mismatches 64
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Matches

REFERENCE AUTHORS TITLE JOURNAL RESULT 3 CD559609 LOCUS SOURCE ORGANISM KEYWORDS VERSION ACCESSION DEFINITION CD559609 CD559609.2 EST. NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
On Jun 10, 2003 this sequence version replaced gi:31585677.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics CD559609
AGENCOURT 14496932 NIH MGC 195 I IMAGE: 6971866 5', mRNA sequence Hominidae; Homo Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homo sapiens Homo sapiens (human) (bases 1 to GI:38558943 sequence. Homo mkNA linear EST 26-NOV-2003 sapiens cDNA clone

CD559459/c

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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencurt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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                                                            CAGCACCTGTCCTCTCGTACCCACGGTTCCGAAGATTCCTGA 405
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/tissue_type="mixed"
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loxP-HindIII; Clones from this_library have been
PCR-amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCBI's RefSeq]. Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxP sites
of the pDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene
Expression Laboratory, Research Technology Program, SAIC
Prederick, NCI-Frederick, Frederick, MD 21702). For
information on which gene each clone represents, please
visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
a Note: this is a NIH_MGC Library."
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/mol_type="mRNA"
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Pred. No. 9.9e-83;
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                                                                                       388 AAAAATTATGTGAATGACTTGGTCCCTGAATTTCTGCCAGCTCCAGAAGATGTAGAGACA 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 581)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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S81 bp mRNA linear ES AGENCOURT 14496771 NIH MGC 195 Homo sapiens cDNA clone IMAGE: 6971863 5', mRNA sequence.
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Plate: IRBK2 row: g
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Tissue Procurement: Narayan Bhat
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Bldg. 31 Rm10A07 Bethesda, MD 2
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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AACTGTGAGTGGTCCGCTTTCTCCTGTTTCCAGAAAGCCCCAGCTGAAATCCCGCAAACACC 183
                                                                                                                                     AAAAATTATGTGAATGACCTGGTTCCCGGAATTCCTGCCGGCTCCGGAAGATGTTGAGACC 123
                                                                                                                                                                                                                                              CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 389
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quality sequence start: 21
quality sequence stop: 581
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         information on which gene each clone represents, please visit our anonymous fip site at ftp://image.lnh.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 9.9e-83;
0; Mismatches 64;
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CD559457.2
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National Institutes of Health, Mammalian Gene Collection (MGC)
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AGENCOURT_14496897 NIH_MGC_195 Homo sapiens
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1 (bases 1 to 582)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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/clone="IMAGE:6971865"
/tissue_type="mixed"
/lab_host="DHSA (T1 phage-resistant)"
/lab_host="DHSA (T1 phage-resistant)"
/clone lib="NIH MGC 195"
/clone lib="NIH MGC 195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
/noxP-HindIII; Clones from this library have been
PCR-amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCBI's RefSeq). Template for PCR is cDNA
derived from either pooled cytoplasmic polya RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxP sites
of the pDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene
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[mol_type="mRNA"]
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84.1%;
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Pred. No. 9.9e-83;
0; Mismatches 64
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Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 2089 Email: cgapbs-r@mail.nih.gov Tissue Procurement: Narayan Bhat \$82 bp n AGENCOURT 14496648 NIH MGC_195 Homo IMAGE:6971861 5', mRNA sequence. CD559461 Unpublished (1999)
On Jun 10, 2003 this sequence version replaced gi:31585529. http://image.llnl.gov Plate: IRBK2 row: g NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Hominidae; Homo. 1 (bases 1 to 582) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homo sapiens Homo sapiens (human) CD559461.2 GI:38453488 EST. found through the I.M.A.G.E. Consortium/LLNL at: CDNA Library Preparation: Bhat Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can quality sequence start: column: 04 20892 mRNA linear ES sapiens cDNA clone EST 19-NOV-2003 ĕ,

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AGENCOURT 14496960 NIH MGC 195 Homo sapiens cDNA clone
IMAGE:6971866 5', mRNA sequence.
CD559456
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                                                                                          CD559456
CD559456.2 GI:38453480
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                    Homo sapiens (human)
Homo sapiens
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Similarity 84.1%;
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/lab_host="DH5A (T1 phage-resistant)"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/clone="Vector: pDNR-Dual; Site_1: loxp-Sall; Site_2:
/note="Vector: pDNR-Dual; Site_1: library have been
PCR-amplified using gene-specific primers to contain the
pcR-amplified using frame (based on known gene sequences
complete open reading frame (based on known gene sequences
available from NCSI's RefSeq). Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxP sites
of the pDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene
Expression Laboratory, Research Technology Program, SAIC
Frederick, NCI-Frederick, Frederick, MD 21702). For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      information on which gene each clone represents, please visit our anonymous fip site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Best Local Similarity 84.1%;
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E 1 (Dases 1 to 583)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

On Jun 10, 2003 this sequence version replaced gi:31585524.

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-remail.nih.gov

Tissue Procurement: Narayan Bhat
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High quality sequence start: 8
High quality sequence stop: 583.
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                                          ACCAACGCAGGTCGTCAGAAACACCGTCTGACCTGCCCGTCCTGTGATTCTTATGAG
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ACAAATGCAGGGAGAAGACAGAAACACAGACTAACATGCCCTTCATGTGATTCTTATGAG
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/clone_lib="NIH_MGC_195"
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/note="Wector: pDNR-Dual; Site_1: loxp-sall; Site_2:
/note="Wector: pDNR-Dual; Site_1: library have been
PCR-amplified using gene-specific primers to contain the
pcR-amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCBI's RefSeq). Template for PCR is cDNA
derived from sither pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/clontech and Washington University).
PCR products are directionally cloned into the loxP sites
of the pDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene
Expression Laboratory, Research Technology Program, SAIC
Frederick, NCI-Frederick, Frederick, MD 21702). For
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971866"
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Matches 338; Conserv
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Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: Cgapbs r@mail.nih.gov
Tissue Procurement: Narayan Bhat
CDNA Library Preparation: Bhat Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK2 row: g column: 06
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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AGENCOURT 14496744 NIH MGC 195 H
IMAGE:6971863 5', mRNA sequence
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On Jun 10, 2003 this sequence version replaced gi:31585680.
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e: IRBK2 row: g column: 06 quality sequence stop: 583.
                                                                                                                                                                                    (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please
                                                                                                                                                                                                                                                                                                                                                         /lab_host="PH5A (T1 phage-resistant)"
/clone_lib="NH5A (T2 195"
/clone_lib="NH5A (T2 195"
/clone_lib="NH5A (T2 195"
/note="Vector: pDNR-Dual; Site_1: loxP-Sal1; Site_2:
/note="Vector: pDNR-Dual; Site_1: loxP-Sal1; Site_2:
/note="PCR-amplified using gene-specific primers to contain the
PCR-amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCBI's RefSeq). Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
                                                                                                                   visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
a Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:6971863"
/tissue_type="mixed"
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                    74.0%;
84.1%;
  0,
Score 299.6; DB 5;
Pred. No. 9.9e-83;
0; Mismatches 64;
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                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: Bhat Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK2 row: g column: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cgapbs-r@mail.nih.gov Tissue Procurement: Narayan Bhat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On Jun 10, 2003 this sequence version replaced gi:31585682.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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AGENCOURT 14496629 NIH_MGC 195 Homo
IMAGE:6971861 5', mRNA sequence.
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quality sequence stop: 592.
Location/Qualifiers
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loxP-HindIII; Clones from this library have been_
                                                                                                                         /mol_type="mRNA"
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/clone="IMAGE:6971861"
                                                                                                                                                                                                           organism="Homo sapiens"
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                On Jun 10, 2003 this sequence version Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892
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AGENCOURT 14496869 NIH MGC 195 Homo
IMAGE:6971865 5', mRNA sequence.
                                                                                                                                  Hominidae; Homo.

1 (bases 1 to 599)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                                                              Homo sapiens (human)
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CD559610.2 GI:38558945
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Email: cgapbs-r@mail.nih.gov
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84.1%;
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Pred. No. 1e-82;
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plate: IRBK2 row: g column: 08
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                             CAGCACCTGTCCTCTCGTACCCACGGTTCCGAAGATTCCTGA 405
                                                                                                                                            AAAAAACCGCCGAAAGAATTCCTGGAACGTTTCAAATCCCTGCTGCAGAAAATGATTCAC 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACTGTGAGTGGTCCGCTTTCTCCTGTTTCCAGAAAGCCCAGCTGAAATCCGCAAACACC
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/lone_lib="NIH MGC_195"
/clone_lib="NIH MGC_195"
/clone_lib="NHH MGC_195"
/clone_lib="Neture: pDNR-Dual; Site_l: loxp-Sall; Site_2:
/note=""Vector: pDNR-Dual; Site_l: loxp-Sall; Site_2:
/note=""Vector: pDNR-Dual; Site_l: library have been
PCR-amplified using gene-specific primers to contain the
PCR-amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCBI's RefSeq). Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxP sites
of the pDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene
Expression Laboratory, Research Technology Program, SAIC
Frederick, NCI-Frederick, Frederick, MD 21702). For
information on which gene each clone represents, please
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
a Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
/clone="IMAGE:6971865"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGENCOURT 14496682 NIH MGC 195 Homo sapiens cDNA clone IMAGE: 6971862 5', mRNA sequence.
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On Jun 10, 2003 this sequence version replaced gi:31585681.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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1 (bases 1 to 600)
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Bldg. 31 Rm10A07 Bethesda, MD 20892
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                                                                                                                                                                                 AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGGCTCCGGAAGATGTTGAGACC 123
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quality sequence stop: 600.
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//lab host="MISA (TI phage-resistant)"
//clone lib="NIH MGC 195"
//note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
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/note-wector: loxP-SalI; Site_2: loxP-SalI; Site_2:
/note-wector: loxP-SalI; Site_2: l
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/clone="IMAGE:6971862"
/tissue_type="mixed"
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/mol_type="mRNA"
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83.8%;
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
On Jun 10, 2003 this sequence version replaced gi:31585528.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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quality sequence start: 4
quality sequence stop: 581.
Location/Qualifiers
PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the lows sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC
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                                                                                                  2 (bases 1 to 489)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
                                                  Direct Submission
Submitted (16-NOV-2003) Celera Genomics,
Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pan troglodytes IL21 gene, genomic survey sequence.
AY417616
AY417616.1 GI:39773576
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                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 489)
                    sequence was made by sequencing based on alignment.
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Location/Qualifiers
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CR988723 RZPD 1
mRNA sequence.
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Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
                                                                                                                                         Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer
Heubnerweg 6, D-14059 Berlin, Germany
Email: www.rzpd.de
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                                                                                          RZPD; RZPDp9016J0144.
RZPDLIB; (Human T-Lymphocytes) RZPD LIB
http://www.rzpd.de/cgi-bin/products/set
                                                                                                                                                                                              Human T-Lymphocytes library Unpublished (2005)
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EST.
                                                                                                                                                                                                                               and Korn, B.
                                                                                                                                                                                                                                             Heil, O., Ebert, L., Hennig, S.,
                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                   CR988723
                                                                                                                                                                                                                                                                            Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
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82.6%;
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Pred. No. 4.8e-81;
0; Mismatches 70
                                                                                                                                                                                                                                                                                                                                                                                                                sapiens
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                                                                                                                                                                                                                                             Henze,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                mRNA linear EST 28-JUN-2005 cDNA clone RZPDp9016J0144 5',
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                                                                 Genomforschung GmbH
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                                                                                            No.9016
.cgi?libNo=9016 Contact:
                                                                                                                                                                                                                                              Radelof, U.,
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AUTHORS
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                                                                                                                                                            ACCESSION
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Best Local Similarity 82.3%;
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                                                                                                                                                                        CD559611 608 bp mRNA linear ES' AGENCOURT_14496808 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971864 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 63
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NIH-MGC http://mgc.nci.nih.gov/
                   Hominidae; Homo.
1 (bases 1 to 608)
                                                                                                                                        CD559611.2 GI:38558946
                                                                                           Homo
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                                                    Mammalia; Eutheria;
                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/note="Vector: pQE80LSN_cloned; Site_1: SalI; Site_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="RZPDp9016J0144"
/tissue_type="T-Lymphocytes"
/dev_stage="adult"
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/mol_type="mRNA"
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                                                     Euarchontoglires; Primates; Catarrhini;
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Pred. No. 1.6e-80;
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Query Match
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On Jun 10, 2003 this sequence vers
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 2089
Email: cgapbs-remail.nih.gov
Tissue Procurement: Narayan Bhat
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACTGTGAGTGGTCCGCTTTCTCTGTTTCCAGAAAGCCCCAGCTGAAATCCGGCAAACACC 183
                                             CTTATGAGAAAAAACCGCCGAAAGAATTCCTGGAACGTTTCAAATCCCTGCTGCAGAAAA 355
                                                                                                                                                                                                                                                                                                                     GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAACGTAAACCGCCGTCC
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CTTATGAGAÁAAACCACCCAAAGAATTCCTAGAAAGATTCAAATCACTTCTCCAAAAGA
                                                                                                                              ACAAATGCAGGGAGAAGACAGAAACACAGACTAATTTCTAGACATGCCCTTCATGTGATT 465
                                                                                                                                                                                                 ACCAACGCAGGTCGTCGTCAGAAACACCGTCT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab host="DH5A (TI phage-resistant)"
/clone lib="NIH MGC 195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
/note="Vector: pDNR-Dual; Site_2: loxP-SalI; Site_2:
/note="Vector: poled cytoplasmic polya RNA from 30 cells lines or pooled cytoplasmic polya RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
a Note: this is a NIH_MGC Library."
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/mol_type="mRNA"
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Pred. No. 1.5e-77;
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